

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I, III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.

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## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 15/12

US CL : 536/23.1, 23.5; 435/6, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched  
NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
NONE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- A	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 ----- 9, 19
X --- A	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analysis of 280,000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828.	1-8 ----- 9, 19



Further documents are listed in the continuation of Box C.



See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

23 October 2001 (23.10.2001)

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

Box PCT

Washington, D.C. 20231

Facsimile No. (703)305-3230

Date of mailing of the international search report

02 JAN 2002

Authorized officer

Marianne P. Allen

Telephone No. 703-308-0196

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with  
10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the  
15 sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

25 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 25 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIQHKTIRPLLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLKF MPRNGTGVLLSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIIVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLYVGVEDKANATVD GLEQGHFVCPSEKRYLLFTFL KKNQKKKLMVFFSACMSVKYP YGLLKYIDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSSEHSNPCHKNLKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTRYSLCPWATKCLKAC FISQK*KRDVIERNASQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGASNLTLSETQNGDVSEET MGSRKVKKSKQKPMNVGLSET QNGGMSQEAVGNIKVTKSPQK STVLTNGEAMQSSNSESCKGK MKKKRKMVNDAEPDTKKAKT ENKGKSEESAETTKETENNVE KPDNDEDESEVPSLPLGLTGAF EDTSFASLCNLVNENTLKAIKE MGFTNMTEIQHKSIRPLLEGRD LLAAAKTGSGKTLAFLIPAVELI VKLRFMPRNGTGVLLSPITRE LAMQTFGVKELMTHHVHTYG LIMGGSNRSAAQKLGNGINIIV ATPGRLLDHMQNTPGFMYKNL QCLVIDEADRILDVGFEELKQI IKLLPTRRQTMFSATQTRKVE DLARISLKKEPLYVGVDDDKA NATVDGLEQGYVVCPSERFL LLFTFLKKNRKKLMVFFSSCM SVKYHYELLNYIDLPLVAIHGK QKQNKRTT\TFFQFCNADSG\TL LCTDVAAARGLDIPVDWIVQY DPPDDPKEY\HRVG*EQPEGLN GEEGHALASFLRPRKDLGFFFR LL*KHSGFPLSGIWTFWS/SLK ISDIQFSAWRNWIGKVITFLHKS A\QEAYKSYITEPMDSPFL*NRS FN\VNNLNLASGLLCQFGFK\VP PFVDLVNNSNEGKQKRGGGG GFGLPRKTQEKLEKSKIF*TH* ARKSSGQAGQFSH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30322	60690	B	30507	1	906	
30323	60691	B	30508	1	2865	
30324	60692	B	30509	45	820	
30325	60693	B	30510	1	783	
30326	60694	C	30511	18	410	
30327	60695	B	30512	1	840	
30328	60696	B	30513	1	945	
30329	60697	B	30514	1	2108	
30330	60698	B	30515	1	2457	
30331	60699	B	30516	1	1156	
30332	60700	B	30517	43	4677	
30333	60701	B	30518	80	964	
30334	60702	B	30519	1	4521	
30335	60703	B	30520	1	2460	
30336	60704	B	30521	1	1854	
30337	60705	B	30522	1	1367	
30338	60706	B	30523	273	419	
30339	60707	B	30524	1	1786	
30340	60708	B	30525	1169	1443	
30341	60709	B	30526	1	486	
30342	60710	B	30527	13	1260	
30343	60711	B	30528	270	723	
30344	60712	B	30529	1	834	
30345	60713	B	30530	1	1632	
30346	60714	B	30531	1	4831	
30347	60715	B	30532	184	1593	
30348	60716	B	30533	1	615	
30349	60717	B	30534	1	3513	
30350	60718	B	30535	113	1666	
30351	60719	B	30536	101	2667	
30352	60720	B	30537	1	1692	
30353	60721	B	30538	51	142	
30354	60722	B	30539	1	3198	
30355	60723	B	30540	251	1207	
30356	60724	B	30541	1	1491	
30357	60725	B	30542	1	4024	
30358	60726	B	30543	1	3316	
30359	60727	B	30544	1	1342	
30360	60728	B	30545	91	810	
30361	60729	B	30546	17	489	
30362	60730	A	30547	1	504	MGGSNRS AEAWKLANGINIIVA TSGRLLDHMQNTPGFMYKNLQ CLVIDEADRILDVGFEELKQII KLLLTHRQTMLFSATQTQKVE DLARISLKKEP/LYVGDDDDNA NETVFGVTLCTDVAARGLDITE VDCIVQYDPPDDPKEYIHSVGR TARGLNGRENWVFFAT
30363	60731	A	30548	1	2676	
30364	60732	B	30549	1	1071	
30365	60733	A	30550	1	348	

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30271	60639	B	30456	1	945	
30272	60640	B	30457	1	7437	
30273	60641	B	30458	1	1122	
30274	60642	B	30459	317	1630	
30275	60643	B	30460	1	1716	
30276	60644	B	30461	46	915	
30277	60645	B	30462	1	624	
30278	60646	B	30463	244	2988	
30279	60647	B	30464	1	804	
30280	60648	B	30465	1	1455	
30281	60649	B	30466	1	732	
30282	60650	B	30467	340	777	
30283	60651	B	30468	1	714	
30284	60652	B	30469	166	1337	
30285	60653	B	30470	72	617	
30286	60654	B	30471	1	1002	
30287	60655	B	30472	1	4173	
30288	60656	B	30473	1	4488	
30289	60657	B	30474	1	3822	
30290	60658	B	30475	1	1866	
30291	60659	B	30476	1	1002	
30292	60660	B	30477	1	1407	
30293	60661	B	30478	99	1046	
30294	60662	B	30479	122	1113	
30295	60663	B	30480	302	4145	
30296	60664	B	30481	1	669	
30297	60665	B	30482	1	933	
30298	60666	B	30483	1	2136	
30299	60667	B	30484	1	4017	
30300	60668	B	30485	1	1335	
30301	60669	B	30486	1	1095	
30302	60670	B	30487	1	2895	
30303	60671	B	30488	1	1215	
30304	60672	B	30489	1	2001	
30305	60673	B	30490	1	1281	
30306	60674	B	30491	1	780	
30307	60675	B	30492	1	858	
30308	60676	B	30493	1	699	
30309	60677	B	30494	1	1624	
30310	60678	B	30495	1	2958	
30311	60679	B	30496	30	658	
30312	60680	B	30497	1	1755	
30313	60681	B	30498	1	631	
30314	60682	B	30499	1	1528	
30315	60683	B	30500	1	1056	
30316	60684	B	30501	1	2305	
30317	60685	B	30502	1	723	
30318	60686	B	30503	1	2691	
30319	60687	B	30504	1	2322	
30320	60688	B	30505	401	2677	
30321	60689	B	30506	1	1218	

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30251	60619	A	30436	1	2607	MLTMSVTLSPRLSQDLDPMAT DASPMANMTPTVEQGEGERA MKDMDSDQYKPPPLHTGAD WKIVLHLPEIETWLRMTSERVR DLTYSVQQSDSKHVDVHLVQ LKDICEDISDHVEQIHALLETF SLKLLSYSVNVIVDIHAVQLLW HQLRVSVLVLRERILQGLQDAN GNYTRQTDILQAFSEETKEGRL DSLTEVDDSGQLTIKCSQNYLS LDCGITAFELSDYSPSEDLLSGL GDMTSSQVKTKPFDWSYSEM EKEFPELIRSVGLLTVAADSIST NGSEAVTEEVSVQVSLSVDDKG GCEEDNASAVEEQPGLTLGVSS SSGEALTNAAPSSSETVQQESS SSSHHDAKNQQPVPCENATPKR TIRDCFNYNEDSPTQPTLPKRGL FLKEETFKNLKGNGGKRQMV DLKPEMSRSTPSLVDPPDRSKL CLVLQSSYPNPSAASQSYECL HKVGNLNLNTVKFHIKEISSS LGRLNDCYKEKSRLKKPHKTSE EVPPCRTPKRGTGSGKQAKNT KSSAVPNGELSYTSKAIEGPQT NSASTSSLEPCNQRSWNAKLQL QSETSSSPAFTQSSSESVGSDNI MSPVPLLSKHKSKKGQASSPSH VTRNGEVVEAWYGSDEYLALP SHLKQTEVLALKLENLTKLLPQ KPRGETIQNIDDWELSEMNSDS EIYPTYHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	B	30438	1	702	
30254	60622	B	30439	1	936	
30255	60623	B	30440	1	1494	
30256	60624	B	30441	1	921	
30257	60625	B	30442	1	3342	
30258	60626	B	30443	1	1072	
30259	60627	B	30444	1	3711	
30260	60628	B	30445	15	674	
30261	60629	B	30446	1	2127	
30262	60630	B	30447	1	3132	
30263	60631	B	30448	103	438	
30264	60632	B	30449	1	3042	
30265	60633	B	30450	1	1425	
30266	60634	B	30451	84	1954	
30267	60635	B	30452	1	1419	
30268	60636	B	30453	130	1615	
30269	60637	B	30454	1	1794	
30270	60638	B	30455	1	3255	

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30242	60610	A	30426	215	1984	LLLVVTMSNNGLDIQDKPPAPP MRNTSTMIGAGSKDAGTLNHG SKPLPPNPEEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE HTIHVGFDVAVTGEFTGMPEQW ARLLQTSNITKSEQKKNPQAVL DVLEFYNSKKTSNSQKYSFST GDKSAHG YIAAHPSSSTKTASEP PLAPPVSEEEEEEEEEEDENEP PPVIAPRPEHTKSIYTRSVVESIA SPAVPNKEVTPPSAENANSSTL YRNTDRQRKKSKMTDEEILEKL RSIVSVGDPKKKYTRFEKIGQG P\SGTVYTAMDVATGQEVAIKQ MNLQQQPKKELIINEILVMREN KNPNI VNYLDSYLVGDELWVV MEYLAGGSLTDVV TETCMDEG QIAAVCRECLQALEFLHSNQVI HRDIKSD\NILLGMDGSVKLTDF GFCAQITPEQSKLSTHG*GTPY WMAPEVVDTERAYGPK/VLDI WSLGIMAIEMIEGEPPLYNENP LRALYLIATNGTPELQNPEKLS AIFR\DFL\NRCLEMDVEKRGFS/ SKELLQHQLKIGQAPSPSLTPH *LLQPKEATKEQSPKTHTHPQP HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL NCLSSYGWTLWWRIALVGA*R SLAPSRGSWSTQARPLKQRRTK WCGKSWCLSGTSEPLSHWPRL RSW
30249	60617	A	30433	16	346	RTDTYHLEDSEKESGNRAGSG GWL*SCAE/GRRVALKSWPGRT MSGTRRV TASSRGTSWYCGG SAGRSSTPPTGRACSPGSFSSPE PQPPGPSAAGSSVSGQLGPCGG
30250	60618	A	30434	1	1772	



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30235	60603	A	30419	97	2012	WADEETWLCLPHLPVFSPTAHL PLLSSTPFSSLLPFISTPHPRGFA LPLPPSARLYLELRKLPATLPWS SVTDGTGSYLSGRRERGGEGEGP GRRVRVADHGFALPRTGPQGS EEELANMQGLIVERLERAVSRL ESL\SAESHRPPGN\CGEVNGVI A\GVAPSRGKPLHLKLMDSMVA EFLKNSRILSGDVETLAEIVHS AFQAQRAFLLMASQYQQPHEN DV\AALLKPISEKI\KEIQTFQRE /RTRGSNMFNHL SAVSE*IPCPL DGI AVSPKPG\PY\VKEMND\AA TFYT\NRVLKD*KQSDLRHVDW VKS YLNIWSELQAYIKEHHTTG LTWE/SKTGPVASTVSI AF SVLS SGA WGFPPPPPLPPPG\PPSTFS EEWK GKKEESSPSR\SA LFAQL N/QGEKAITKGLRHVT\DDQKT YKNPSLRAQGGQTQSPTKSHTP SPTSPKSYPSQKHAPVLELEGK KWRVEYQEDRIDLVISETELKQ VAYIFKCEKSTIQIKGKVNSIID NCKKLGLVFDNVVGIVEVINSQ DIQIQVMG\RVPTIS\INKTEGCH IYLS DALDCEI\VS AKSIWKWN ILYPPQGWVD\YREFPHFPEQF KTS/AWDGS\KLITEP\AEIMALT SLRDRTSPESP SIKTNKKA AVK
30236	60604	B	30420	1	499	
30237	60605	B	30421	390	851	
30238	60606	B	30422	136	603	
30239	60607	B	30423	1	2190	
30240	60608	A	30424	82	242	
30241	60609	A	30425	1	330	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30232	60600	A	30416	645	2571	GRPRLFPQLFPPNPPVFRGQHPR QGLGPPSAAGRRAMKKKLVVL GLLAVVLVLVIVGLCLWLPSAS KEPDNHVYTRAAVAADAKQC SEIGRVLVGGPAYLLLLGKAEV INAREVAPRLAFASMFNSSEQS QKGGLSVAVPGEIRGYELAHQ RHGRLPWARLFQPSIQLARQGF PVGKGLAAVLENKRTVIEQQPV LWYVCGKVLREGERLTLPLRA DTYEMLAIEGAQAFYNGSLMA QIVKDIQAAGGIVTAEDLNNYR AELIEHPLNISLGDAVLMP RLSGPVLALILNILKGYNFSRES VETPEQKGLTYHRIVEAFRFAY AKRTLLGDPKFVDVTENSIAGL LCARMDSPALGSRQVVRNMTS EFFAAQLRSQISDHTTHPISYYK PEFYTPDDGGTAHLSVVAEDGS AVSATSTINLYFGSKVCSPVSGI LFNNEMDDFSS\PAFTNEFGAPP SPANFIQPGKQPLLSMCLTIMV GQDGQVRMVVGAAGGTQITTD TALPPSHADHTPMPQAIHYNLW FGYDVKRAVEEPRLHNKLLPN VTTVERNIDQAVTAALETRHH HTQIASTFIQVQAIVRTAGGW AAALDSRKVPTPGAGFWGLV EVGWWEAVITAQHLDITRGTG
30233	60601	A	30417	5	439	
30234	60602	A	30418	1	423	

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30229	60597	A	30413	110	868	DLCPLPTLPPHLLRPALGSRQV VRNMTSEFFSAQLRAQISDDTT HPISYYKPEFYMPDDGGTAHLS VVAEDGSAVSATSTINLYFGSK VRSPVSGILLNNEMDDFSSTSIT NELGVPPSPANFIQPGKQPLSS MCPTIMVGQDQGVRMVVGAA GGTQITMATALAIYQPSWFGY DVKRAVEEPRLHNQLLPNVTT VERNIDQAVTAALETRHHHTQ IASTFIADVQAIVRTAGGWAAA SDSRKGGEPAGY
30230	60598	A	30414	1	1626	
30231	60599	A	30415	171	2097	PSGEREGCLIRESLKKILWLQAS AECEGDPGYFLSYFHQILLSFV ANTPRQGLGPPSAAGRRAMKK KLVLGLLAVVLELVIVGLCL WLPSASKEPDNHVYTRAAVAA DANLCSKIGRDALRDGGSADV AAIAALLCVGLMNAHSMGIGG GLFLTIYNSTTRKAEVINAREV APRLAFATMFNSSEQSQKGGLS VAVPGEIRG\YELAHQRHGRLP WARLFQPSIQLARQGFVVGKGL AAALENKRTVIEQQPVLCVFC RDRKVLREGERLTLPQLADTYE TLAIEGAQAFYNGSLTAQIVKDI QAAGGIVTAEDLNNYRAELIEH PLNISLGDAVLYMPSAPLSGPV LALILNILKGYNFSRESVESPEQ KGLTYHRI\VEVFRFAYAKRTL LGDPKFVDVTEASSGVSA\VVR NMTSEFFAAQLRAQISDDTTTHPI SYYKPEFYTPDDGGTAHLSVV AEDGSAVSATSTINLYFGSKVR SPVSG\ILFNEMGDLSSPS\TN EFGAPPSPANFIQPGKQPLSMC LTIMVGQDQGVRMVVGAAAGG TQITTDALAIYN\LCFGYDVK RAVEEPRLHNKLLPNVTTVERN IDQAVTAALETRHHHTQIASTFI AVVQAIVRTAGGWAAAASDSRK

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30226	60594	A	30410	604	2475	RQREVTRSPPPERSGLRVLQLFPP NPPVFRGQHPRQGLGPPSAAGR RAMKKKLVLGLLAVVLVLVI VGLCLWLPSASKEPDNHVYTR AAVAADAKQCSKIGRDALRDG GSAVDAAIAALLCVGLMNAHS MGIGGGLFTIYNSTTRKAEVIN AREVAPRLAFATMFNSSEQSQK GGLSVAVPGEIEGYELAHQRHG RLPWARLFQPSIQLARQGFPVG KGLAAALENKRTVIEQQPVLC VFCRDRKVLREGERLTLPQLAD TYETLAIEGAQAFYNGSLTAQI VKDIQAAGGIVTAEDLNNYRA ELIEHPLNISLGDAVLYMPSAPL SGPVLALILNILKGYNFSRESVE SPEQKGLTYHRIVEAFRFAYAK RTLLGDPKFVDVTEASSGVSA VVRNMTSEFFAAQLRAQISDDT THPISYYKPEFYTPDDGGTAHL SVVAEDGSAVSATSTINLYFGS KVRSPVSGILFNNEMDDFSSPSI TNEFGVPPSPANFIQPGKQPLSS MCPTIMVGQDGQVRMVVGAA GGTQITTATALAIYNLWFGYD VKRAVEEPRLHNQLLPNVTTVE RNIDQAVTAALETRHHHTQIAS TFIAVVQAIVRTAGGWAAASDS RKGGEPAgy
30227	60595	A	30411	63	342	GRTLVPHGGLPHHYLVQCEWL PGTS*AEFPVVHLPAFVARARG ADRQHHGPFLPLCHLHPARPRR EDLHRKSPGEPNPIEHHRSSGPG CRRI
30228	60596	A	30412	1	910	MLFRPALGSRQVVVRNMTSEFF AAQLRAQISDDTTHPISYYKPEF YTPVDGGTAHL SVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN DEMDDFSSPNITNEFGVPPSPAN FIQPGMGWRKQPLSSMCPTIM VGQDGQVRMVVGAAAGGTQITT ATALICVTAFLPGRAHPAQPPS HADHTPMPQAIYNLWFGYDV KRAVEEPRLHNQLLPNVTTVER NIDQAVTAALETRHHHTQIAST FIAVVQAIVHTAGGWAAASDS RKGGAyrILSALQEDKADKQS RDKILTRTRKGTLDGWLPM

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30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ LLKNLINPSCMVRRAEEIYENI PGLCKTTFLDDAVRNRAGYE VRQMAAALLRRLSSGFEEVYP NLPADVQRDVKIELILAVKLET HASMRKKLCDIFAVLA\RNLD EDGTNHWPEGLKFLDSIYSTN VALWEVALHVFVWHFPGIFGTQ ERHDLDIKRLLDQCIQDQDHP AIKTL SARAAAAFVLANENNIA LFKDFAD\LPGLQAVNDSCYQ DDDSVLESLVEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRCNPPPPAHSDTTGKDSF GNIRGAETGQGASACSVTSARV TCGAGSEPHSHRNPGISAQVGL APSYGAARGRRRPLALQQSPQE RRHVGWNSTRGLLPASLPGTAS SQSASATASAALPLKVTGPLAR NPTPPWTA\AAALATRGQRPEK GLFPGPAPFSLGKRKRGRGRTW ERRRRVSIETSTCFRPGCERLGA AAGANLSQLASSQRPLRERWV LYTIIMAAAGAPDGMEEPGMD TEAETVATEAPARPVNCLEAEA AAGAAAEDSGAARGSLQPAPA QPPGDPAAQASVSNGEDAGGG AGRELVDLKIIWNKTKHDVKFP LDSTGSELKQKIHSITGLPPAMQ KVMYKGLVPEDKTLREIKVTS GAKIMVVGSTINDVLAVNTPK DAAQQDAKAEENKKEPLCRQK QHRKVLDKGKPEDVMPSVKGA QERLPTVPLSGMYNKS GGKVR LTFKLEQDQLWIGTKERTEKLP MGSIK\NV\SDPIEGHEDYHN DGRFQLAPTEA\SYWVYWVP TQYVDAIK\DTVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP SAAGRRAMKKKLVLCLLAVV LVLVIVGLCLW/LPSASKEPDN HVVTRATVAADAKQCSEIGRK\ AEVINAREVAPSVAFASMFNSS EQSQKAL
30225	60593	A	30409	562	2376	

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30204	60572	A	30388	1	425	MDQIISLFGRPDHVAYDIRSLRN KANPDDTFEAQLFYGDLKAIVK TSHLVKIDYPKFIVHGKKGFSIK YGIDQQETSLKANIMPGEFGFA ADDSVGVLEYVNDEGVTVREE MKPEMGDYG/PRL*CVVSNHHP RCAKLRQGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPRGRDTCGPCRC KQNSTCIAAVKMEGPLSVFGDR STGETIRSQNDKESFNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS IANIVKSSLGPVGLDKML\DDI GDVTITNDGATILKLEVEHPA AKVLCELADLQDKEVGDGTTTS VVIIAAELLKNADELVKQEIHPT SVISGYRLA\CKEAVRYINENP NLLTQDELGRDCLINAAKTSMS S\QIIGINGDFFANMVVDVLA KYTDIRGQPRYPVNSVNILKAH GRSQMESML\ISGYALNCVVG QGMPKRIVNAKIACLDLQKT KMKLVGVVITDPEKLDQIRQR ESDITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLKRD\KRIAKASGATILSTLA\ NLEGEETFEAAMLGQA\EEVVQ ERICDDELILIKSTKA\RTSASIIS RVPIDSMCDEMERSLHDA\LCV VK\RVLESK\SVVPRIGGAVEAA LSIY\LENYA\TSMGSREQLAIAR VCKITLWLPNTLSS*CLPRDST DLVLQNLRAFHNEAQV\NPER\ KNLKWIGLDLSNGTPRDNKQA GVFEPTIVKVRGLNFATEAAITV LRIDDLIKLHPESKDDKH/G/GS YEDAVHSGALND
30206	60574	B	30390	1	975	
30207	60575	B	30391	1	2577	
30208	60576	B	30392	1	3126	
30209	60577	B	30393	1	1134	
30210	60578	B	30394	1	2082	
30211	60579	B	30395	1	915	
30212	60580	B	30396	1	2658	
30213	60581	B	30397	1	2412	
30214	60582	B	30398	1	2454	
30215	60583	B	30399	89	2533	
30216	60584	B	30400	1	4083	
30217	60585	B	30401	1	1725	
30218	60586	C	30402	127	345	
30219	60587	A	30403	1	597	

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30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	A	30357	1	420	
30174	60542	A	30358	1115	1561	
30175	60543	B	30359	501	555	
30176	60544	A	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	A	30362	1	1179	
30179	60547	A	30363	1	1215	
30180	60548	A	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	A	30366	1328	1978	
30183	60551	A	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSTNKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRMMYTVTLSSFSANKNTYI *E*E*GLGWRHHIFLG*IQHFN
30187	60555	A	30371	842	905	
30188	60556	A	30372	784	3453	
30189	60557	A	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSGSLGP RGGRGGCILRPSRGGRGRHGPT KAGPWSPESRGR*DWKARGPP APSRGSPSRARARRGGSGGPA DEPGLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	A	30376	2	3336	
30193	60561	A	30377	22	419	
30194	60562	A	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECWSLF*SH MHVLLPRNRKEKLEIFRTQTY DVNAYKASAHNSGPG
30196	60564	C	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	A	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	A	30387	176	1553	

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30152	60520	A	30336	860	1209	IPGNCRDSSGVGIKERETNAGS QHHM/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	A	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	A	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLFRMGMF VKVVKNKAYFKRYQVKFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIVRVTNRDICQIAYA RIEGDMIVCATYAH\ELPKYGV KVGLTNYAAAYCTGLLLARRF L\NRFGMDKIYEGQV\ELTGDE YNVESIDGQPGAFTCYLDAGLA RTTTGNKVFGALKGAVDGGLS YPLTVPKRFPWF/DDS*KPRNLI AEVHRKPHPWAQNVARLHAPT LMEED\EDA\YKKQFVRQYVKN SVTPDMM\EEMY\KKAHAAIRE ESSSMEKKAQGKKFKKKRWNR P\KMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	B	30341	1	2043	
30158	60526	A	30342	390	1180	
30159	60527	A	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISEILATRGAVNI TTVAYKSAVILSFTTASAVSLSS RNVIGPLFASQPSFTIHFSLSHN GSAPLNAPDMANCFGLTALTSS LDERLFSRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	B	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	A	30349	439	555	
30166	60534	A	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAKSIADELMTGCTN FAFSGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRVGM\LTNLNY EAMKTLLGERIMDRMTMNGG RW
30168	60536	A	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	



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30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPTFRT PVHYAAFS**/HALGHLAFS/EA SLHSHRGTQALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASLMQ*MHYGKLCFAFQSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNWWQCWPHWTLCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLCWTQSWWLCW SHWRSCWTQSWWLCWPHWRL CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPWPWPSPGSPGLGCSAWAEA PPAHCPDVLLHLHPACPHIQAP CGTGAPGTGLAAAADSEPLGSS APPAGRPCPQAAAACGLAPPLP RGWCPPPTSSWMGRRLQSLSA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTPAPAS SPAPATSPAPAESPAATASHPV AEASPAGAPPPRPAASPSPAAS PAPPAASPVLTASPPLPAASPAL AASPVHTASPPVHVASPPVHTA SPPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQPGAVFP HSL/VSFRLWLVS SSCSTLDGP AGGCGARGSAVWFLSLNKLLP/ MLLYQMYLMLLLLLRCANQ*I DVFSELTDYCGA*IQGYC*FLV LAIPR*VVTTTRSGCVRATAIDFL FPVSSCWNARALPLPICF
30142	60510	A	30326	929	2910	
30143	60511	A	30327	1	1488	
30144	60512	A	30328	203	701	
30145	60513	A	30329	493	924	SDPGFRHGKARITDPRGQPGRR LQGSSENGSDMKAARKVSG NKHSTSSHQHAVWCPGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRNHLSSVSLNGE NQRFGVDARYRTRLQRGSANL FKRQRCGTLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRHRW*FHLVQRH GRFSRASGATWPASAAFAWP LLVCAPLSAASAAPLARL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	

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30132	60500	A	30315	1	468	MTEKVKQQPAPVTASDEIDIGR LVGTVIEARWWVIGITTVFALC AVVYTFFATPIYSADALVQIEQ NSGNSLVQDIGSALANKPPASD AEIQLIRSRLVLGKTVDLDLDI AVSKNTFPFIGAGWDRLMGRQ NETRRGFSARGTGQMLKKEGV TLMVEAIHASPGSEFTVTKYST LGMINQLHNSLTVTENGKDAG VLSLTYTGEDRYTNHAGVVNT MIIIAATHNLVFENNCEY.AHP MGNAPAGLTEYQNVFYKHDRI QGHYVWEWRDHGIAQDDHG NVWYKFGGDYGDYPNNYNFC LDGLIYSDQTPGPGLKEYKQVI APVKIHARDLTRGELKVENKL WFTTDDYTLHAEVRAEGETL ATQQIKLRDVAPNSEAPLQITLP QLDAREAFNITVTKDSRTRY EAGHPATYQFPLKENTAQPVP FAPNNARPLTLEDDRLSCTVRG YNFAITFSKMSGKPTSWQVNGE SLLTREPKINFFKPMIDNHKQEY EGLWQPNHLQIMQEHLRDFAV EQSDGEVLIISRTVKPRGPAPCP DSSVGTTYCTENNPPFDNGLLN AQLLQQA KPFVDERQSK*FGCH SPSYSCLWLSIIGLKKLIFGSRVS SDSPFTCQDVGLPLIFEKVIACL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCPLRKNQGPVRSCGAW GCLWLPSPSGTPWRSSLWILL F/SQISQLLSLLHQGFQPKPNH RGNKYLA KPGGSRAIPD TDGP SARAGGQTDPEQEEGPLDPEED LSVKQLL
30136	60504	B	30319	217	368	
30137	60505	A	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	A	30323	1	2437	

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30126	60494	A	30309	153	2031	RRNYQRQQKRGSEGAGRDPDR RSRISAAYSRSEFNNAAVTEH Y*NRF*TLVPRSR/HANADTVT REAVNQVIALLD SGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPRRCEEKQYMVL MIVSGRSGSGKSVALRALEDM GFYCVDNLPVVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLFLDADRNL TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLEPLHGFPDYDTV GFSCKRRIDYVCRIKHRRIRQV VLLNFAKSGAFSTTRGTDDKTR RSLLVTLVRFCVRVIFAYDIRD GIHVRIIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGKPDQVEQYYIDK VPFKRGCDYQDVLNMLLFYAS PKAVVLAPDSRSMSPAVSGRFK PRVVVAIALDDQQRIVDTLFMK GLTVFARPQKIPAITGRHSGATL QKQGKCSVEELAQYFDTTGTT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWFD NIRSAEFHHVTLLAEIPRQOND IHRPAHAAAAPKVETRSGDETN RRWNRPAQHLFA
30127	60495	A	30310	720	872	EKVPVSI GPGGMQELPMQSPDR RSAGKPGPASRAGR* TGGGAFS TKRDYR
30128	60496	A	30311	1967	2452	SRRCASINQRPRPGHEKMVS RIAPASNVPTCRPITVTGSI SAWTIITRMVSPALARAVRM*S SPSTSSIEERVIRMTASGIVPST MAGKIIWATASIKLPSPQMAV SISIKPVNGLESSRNTISLTRPET GVRFQCTETSMISIMPHQIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRKVST*SVLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAFGGHCEHHQWVSSVSRVRV SQSAGGCPLFNILLNTV
30131	60499	A	30314	1	300	SVFSH*AKKIWKGVSRALGQ NSRSGSGGCQASWTIRFPVGFH TDGTRLRRNPGMQAFLGPVAR FLALEARSLDCAFSSLLFKRKL SGRWGRASRGTKL

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30116	60484	A	30299	3	421	QRRATGDLRLPTR*TARRGGRC DS*SSRRWHRAFTGACREISRQ QNRHRQRPAAGGVALVGSE*T SGILAGQRHYRVYRAGYRRSP AGYAPD*SD*RPVDGRHECGRR PVWRRENVDPATGGQIGARHET GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	A	30301	317	554	
30119	60487	A	30302	474	599	TTSVQRTFLPDY*APTPVLLPA RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSLKVVTPALRSMPSVPINNLS KVKCSKAFAASCP*NEADFLRN VPPGIRIVCSLSSSDSALTICRLL VITVMLLKRESRGITCKTVLPAS RMIESPSWIKLTAASAISFLWV LMSVL
30121	60489	A	30304	1	160	WSKMSRAVRPSDWESWTQTRE VVRQTVRCRDPDPSAAVCLTAS SPANCGIPIG**MLAEILA*RAV RPSDWESWTQTRVVVRQTVRC RPDPPSAAVCLTASSPANCGIPI G
30122	60490	A	30305	1	975	
30123	60491	A	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL GLGARLYRYGADWFCADGGM SAEELKFISENGAVVDMDHKKP GSAAASGPKLHYIKQLLSNRM MLGVFFGQYFINTITWFFLTWF PIYIGNVVSDNR*YVAQITFITW IKTYGRCPSPQRDGDGFVNRCL

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30103	60471	A	30286	737	1088	NMLMNVCNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRCLPIIVGR RKSGGSKIRANVCSLPIFPGIG R*TTGESKRLCRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAEST\SPLAMVGD GINDAPAMKAAAIGIAMSGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQNITIALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFI VGTSGLFNHAENIDEAW RVMTAQILAAKSEQWGQVY AIVQNTDQAQAVMPYGPCKLY VLAQNDALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRWCSDFEFC CDNGERLRVTFALDCCDREAL HWA VTTGGFNSETVQDVMLG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHRPAPALRYPQLQ MPHWRRSICTSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKASLS*FK*LLKPAINAG*Q AS*WRASASKPCSASPDACAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	A	30294	1246	1300	
30112	60480	C	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCGVD
30114	60482	B	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

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30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPHYGRWPQ HDFPPFKLRPQSVTSRIQPGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRTVVAHVFG RSLFTGP*RERFATQIEVGKLF AAVDMVLWLSGKAQPD TVVV KVVVL
30082	60450	A	30265	3174	4135	
30083	60451	A	30266	1	2771	
30084	60452	A	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGIHLPTT DKAPSPLTVDGAK*EVSRSI/R QNSQVQHPPDAAKYPSGCHKS FRGFRA
30086	60454	A	30269	300	564	SANSTLKRTQVNRRLTVKLSA RKLPMKVNTRNSLVVVSMV MLLSTCTRWSRVQTRKATSSST TLKV*SLANTSRLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	A	30271	1	819	
30089	60457	A	30272	1173	1369	
30090	60458	A	30273	1	4767	
30091	60459	A	30274	905	1162	FSSVVMCSSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSCRSS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	A	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGVS RLYAANQHRTCQ
30095	60463	B	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQPSK TLR*HRCTTRALTSGVLAVRLS AGCNFPPELVHRLTLWRAGRT YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLTP PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	A	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	A	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGS LG PSSGPKTAGAPSSRPPSPSARRP RTTETRWTLRSKDYWLITRKV GLGNLQDGGGRAGSL

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30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRLFIGAERFQHIAGSGHYR VV*NANAGSKIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTTENRIRK LCFNLTNTGTQRKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	A	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	A	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPLPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDRPRLAIRDATIGISG FCSLA
30071	60439	A	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCSRWSARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPTHISTDHQG QFVFGSYNAGNVSVTRLEDG LTMLHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPEA CTTNKQPAQPQRDKPQRGNQQ RLASVIFQCQHDHEHKERHTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	B	30258	1	2655	
30076	60444	A	30259	67	231	
30077	60445	A	30260	1109	1531	TFLHSIPAAKTQGPPRNTLVDT PQHL*HQQRRTRQPQLALSLRT *VFLNRILRGALFAPKACLKPD LVISPRGPPQGLGVTRVQVSAH TNPRTTHRNTPHYTRNTQTRPE STPRRDTTTPQQRHTPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLR M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLRM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVITSPQVSIRSR ANPSCTSPFFV*SATKGLLYQQ TRIPALDIPSSNRRNSHG

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30044	60412	A	30227	862	1453	SFLLVSPSQACHHYAP/KIFDL/SGYTSTTEQMWGTVIVGLTNV LATFIAIGLVDRGLFLAMPAGM GVLGTMHIGIHSPSAQYFAIA MLLMFIVGFAMSAGPLIWVLC EIQPLKGRDFGITCSTATNWI ANMIVGATFLTMLNTLGNANTFW VYAALNVLFILLTLWLVPETKH VSLEHI/ERNLMKGRKLREIGAH D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCPPVS VHFFFHSRLCRDALNEAFHPSG FQVVKCCDIARIHRNRYGDLF AIGVVHIANVNAIHRNATFHQR QEIGGCFTNQDFLSIGGAMNV VDNFLQRPETYGDPFCQYHFH QVLLYRIFGNLIVGYQHQCPR KSDPLNADLTVNQAFINPA*NN IWHSVFLFVLLIGLHRLCGMRQ DVLNMVDNEFPWRWLQLAGA NFHVLQRQILADQRQRNW
30047	60415	A	30230	2553	3845	
30048	60416	A	30231	1	656	
30049	60417	A	30232	3	228	
30050	60418	A	30233	185	206	ATVDPPFITEPGDILAGGFA*PL SWFAGFALEHHNLPWATGDLH SLRA
30051	60419	A	30234	12	155	
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	B	30238	1	7521	
30056	60424	B	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPNRKPVLVIP*K WKLKGPVALKTAYPAKRLPLPI TSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	B	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	A	30244	1	1917	
30062	60430	A	30245	239	469	KRVSISSRRRFSQAQKASASALA RWWRSVNIYVFAI*TTAQRV* QLRMTNCRVTTITACHSR*RTL SLSPVKPAS
30063	60431	A	30246	1	4348	
30064	60432	A	30247	1141	2244	
30065	60433	A	30248	503	649	



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30027	60395	A	30210	61	641	RHKHRRRIPGRWDQIRPAPNR WQTGFQWFALPVTGVRLLISGY TELLPRL/PAQKNLPYTIHPAWR FVAHQGRESALECRYVPLPVRH *RNCRWREPRNVDVAEYRRDC GSRFRSLRHFYRSLFSLHRPAST RHPGAQTGAVTGFADECPARK AAALAKASVNVKVVFHSTNATV CHRPDRSRRASGSFRRYWRQE
30028	60396	A	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLANSKNKRR WRKNIKLR*SSLLK*TESPLPMA ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH VILRRTDWMDGRRSRHTDDT DVLLRIHHVIGELPTYGYRRVW ASSQTGRT**FKVQNRYPFPVLS DFEHLQEPYEFYFGKLR*PWLPA TGEFHAIEYRSVD FCKHPV
30031	60399	A	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPCCRKGKRWLFRNHSSARR PTVLYYRRSTMR*NSW*PNLRR QRGNPANRS/RQSMLELSGVKD GELIPAKLFNHLVTWLQARQTL SQQNTPRPGGEIPPWCSSVLA ESERKKRGRKKQRGIDSPDVGA LLVVRATFYIWQPPVNKIALGI EYAASKYYGWQRQNEVRSVQ EKLEKALSQVANEPITVFCAGR TDAGVHGTGQVVHFETTALRK DAAWTLGVNANLPGDIAVRW VKTVPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	A	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	A	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	

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30015	60383	A	30198	1	702	
30016	60384	A	30199	36	144	DGLLLMDERNISPLLQKRMP* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPNMPACHVQRRTSSL ERRQPVMLMVMLRILWYIYCSI HVLG*WICRLYYKTLLK
30018	60386	A	30201	107	1200	
30019	60387	A	30202	366	500	
30020	60388	A	30203	1	1193	LADCSRYNGLEMTLSCCAGAS TDAVGGIERGGLKSPEASEGEI APRLLLDGEPLAELSGDKWRISP WLLVTDDTATITAFQMIEGK AITLRDGDQTISLSGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTPL SLEERNLLDYGNNWRMNGLR SLDPLRREVNTALTDDKALM MISSQIFNGHMHVHIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLVMHHDMTFLRLPHHVE NAGVIIHIEIEINFHPALVGVTRH GVPLVTRSQRQPHTRLAGFQY IRDQIFVNRATVTGEEIAYALF TNFPANGNRFSYRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQLGLIQRFCVRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	A	30205	1	955	
30023	60391	A	30206	1281	1370	
30024	60392	B	30207	1	2199	
30025	60393	A	30208	1	589	MLKKREQTVTFHEKSVFQGLD RGNRELGPCKTFGVKGAQKGN LQIFSEDKNFGPGSGEIWGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLGSFGPWERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDVAEYRRDCGSRFRSL RHFYRSLFSLHRPASTRHQKAQ SSAVTVLQTNQHGRRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRCCAPLSSVWRCR PPRSSPWPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCLWTSSLAPASRP CPS*VLQPPGQQRWGEPIGAIAV PL

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29996	60364	A	30179	404	1347	DVTILARAVLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANLDDLVDV VMIIHDGAFSGIVQNWLMNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAF RVEDVRHTITPQLSTEDNALLLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDRLI
29997	60365	A	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVSKAFSAGSCSILTVT NARASARSACIISITAAVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVLPASPPRIA
30000	60368	A	30183	535	661	
30001	60369	A	30184	1	1491	
30002	60370	A	30185	1400	1852	
30003	60371	A	30186	199	534	
30004	60372	A	30187	2	539	
30005	60373	A	30188	1	690	
30006	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLCL TDERTRR\NNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLRSVPTSTVWTGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSDQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AEIPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNINPLSSVQ CRQNHQAIPCRIFELNVMRH/ VTRDSSSGLGCSWRLTASVNAR RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	A	30197	141	229	

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29983	60351	A	30166	1	1661	MRGEVLLAGVPRHVAEREIATL AGSFSLEHQNIHNLPRDQGGPN TVSLEVESENITERFFVVGEKRV SAEVVAAQLVKEVKRYLASTA AVGEYLADQLVLPALAGAGE FTVAHPSCHLLTNIAVVERFLP VRFSLIETDGVTRQLLGVSYRIL AMGHAEFLIQIADMRNDGGWR DFQFSGNLVMDEPNRSAQTYIK LVKSRLGTTKRYNHKDDCPRC RWIAAMIDNPPRIRKPTKSASV WHATATSASPERQMSTTVIMS ARFISCVWMTPFMPSRSGPMRF VHLPCRFRDAFNTGVGKLDQL GPSMSTRIRQRFTTLCPMTLSSS STEFENVSDCRPSRARSCLRFRL CRSIRCXYRLADYVQVRSQAGF IQRPAIRHPYHHVKGAFTYVVR NNRLPETVIRVLQPALARFSPDI APLSPFPLHDDVTRALYAPS LMPKLRLIGLTLALSATAVSH AEETRYVSDENLTVWRSGPGD HYRLVGTVNAGEEVTLLQTDA NTNYAQVKDSSGRTAWI/HVET T*H*AKPALPCARSGKSGQNP R*THQYR
29984	60352	A	30167	254	496	RASRLKTCGDGCCSLSAVVSVG ASPFASRVKSSRRWV*S*VGPS WPPGMSL*TAEIRRSRRIPVVSS GSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	A	30169	1	429	
29987	60355	A	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	C	30175	1	2649	
29993	60361	A	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

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29978	60346	A	30161	1	4342	MTRDNPVIPRFIHRREVVFQGE NGGIQNARFIAALFFQHGVNLC QRVGGLLKIGIGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNDGRS VTDDFAPDGQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYTGNVALLKGRSNYLC LERLEQQALAGGDLVPQILSDV ILLRSWSNQTVDGDISTCVSVA EDSQA WPLVTSTND
29979	60347	A	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP YDNDGTGPYAFNKTHPKDNYT CTVLFIDDMSASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDLAEQAIR LQDCVFDQTETMTTFTGTVSS ANSGNYYTIFNTDTGA AFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	A	30165	1	1353	

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29951	60319	A	30134	66	413	HQSEQMYQSSESCLLGTTAKA RGHQLRTASACHFPSTPPFWSL TLESQREGRFKQPTLISCF/CLF MSVPVVSAPPFSSSSSSSSSSSS SRPWFPDQEAR*LTSPVERPCR GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCPPVW EVEGHSV*TGKPDPRPPRRKLLT LLLPVPWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	
29954	60322	A	30137	33	265	
29955	60323	A	30138	114	560	
29956	60324	B	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	A	30141	374	575	
29959	60327	A	30142	1	1095	
29960	60328	A	30143	1	981	
29961	60329	A	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP LKSSQH\LRVLNPPNLDGRRKI A\FAHHCPFKGVG\RRYA\HVVL RKAD\DLTKEGGENSLEDEVE RVITH\ILQNPRQYK\IP\DWFLN KTRRM*KDGTYSPPG*PIGLGQ QAPVKDLGAD*KKIRAH*/RGL RHFLGAFRVRGQAHQEPLGRR GRHPSGVSKEEIRSVGPCLVNKI VYIPKKKKKKKKVDAANLVV VVVVGGR
29962	60330	A	30145	107	340	
29963	60331	A	30146	428	934	
29964	60332	A	30147	1	1533	
29965	60333	B	30148	1	2652	
29966	60334	A	30149	205	450	
29967	60335	A	30150	1	879	
29968	60336	A	30151	139	1029	
29969	60337	A	30152	237	422	WFETPAQYTNRSPESGTHYRRA RSRARWHGCMECVCRRRKSPR ANKPRRLPPVR*RCPPRA
29970	60338	A	30153	1	1134	
29971	60339	A	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGWRPAVRVFRWWK PLTVPPRRKGPLSRGTGCRPVPL TTPSTGTVMRAGICAVKMLIVQ KSPCMPPC*HRQWTMTGLWQA PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
29976	60344	A	30159	308	749	
29977	60345	A	30160	1	1338	

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29936	60304	A	30119	1	1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGALETSAAN AGQISPGYAAPWAAPGVPLKAI KWMFQRHAPLAVRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRAPTLNTMPIFKA CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTNVIV YMIQSISLVDEMSCHLVLTGG- TGPARRDVTPTDATALVADREM PGFGEQMRQISLHFVPTAILSRO VGVIRKQALILNLPQPKSIKET LEGVKDA/EGVPYCIQLLEGPY VETAPEVVAAFRPKSARRDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHFV ATTCNRALSIWYLMN
29941	60309	C	30124	202	321	
29942	60310	C	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	A	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLLGPVWPCVSEWSK KPSPRGGDRPSDRDPAFAARS TVPPRISAYERPVWPGEWNDP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGAVTTSQIPASEQET LVRQESSEDYSQP*LLVALFIAA KKM*KSLKGKKPKTKRVWN LVCPLMPLNLV*FVKVDLKMV ALSMKQDILWPALH/DAKKL KKRNKPCPVCRCQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	A	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA\VTTS QIPS/SPEQETVR\PKPLL\LKLL KSVG\AQKDTYYYGKRFLFNLG QYIYGLNDYY
29949	60317	A	30132	3	619	
29950	60318	A	30133	123	385	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTPSLSVCWRPAAKRPILPRS LKQLKKIASRKVTP*/SLGNAW NNLEKQRAYLSMMAQKRVDG LLVMCSEYPELLAMLEEYRHI PMVVMĐWGEAKADFTĐAVID NAFEGGYMAGRYLIERGHREIG VIPGPLERNTGAGPPCRFYEGD GRSDDQVDGDIQFFSTNTITGR GHFRMTVDGICPCKDGNLRFN RILEHREPFYPQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVOIQ QCRFALIFKDFCRMHRNGLIRR TISQQSVGRIRCVSISGRVYYC FFALEGKKPSSSISAAPTQMAVS ARLKVAKCQSPT*KSIISTTKPC HRRSNRLPSAPPIISATRVHRQM RYSTSSGAAALLSITVTPS
29930	60298	A	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTS LLTSVV*IDAIDGIRSFSLSWAS GKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRR RREREKTSERTPAPV*VKITTRK LYPAEERTGRIFEA
29933	60301	A	30116	1	3095	MDKFLNTYTLRLNREEVESLN RPVTASGLEVIINSLPIKKSPGPD GFTAAFYQRYKEDAGEREGEG GNQQVAVRGKRKTTERKKKLG EDVKVKESKNSGAYEVKQHRF FRSLDWNSLLRQKAEFIPQLESE DDTSYFDTRSEKYHHMETEEE DDTNDEDFNVEIRQFSSCSHRFS KAAEVSTRLLSTRVTEIEGWLI VQRNQKLLQSNLKQRSGEPLIL DDDSHVPPELRAGYRLKNAG CLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	A	30118	1	3141	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29904	60272	A	30087	3	264	TLRPANRF*HIPDAAGVIPVGY AL*RGTSVSAVHRW/CSTVFGV NWATLATKLMVAGIRRSAAS RISRASPPSFSVPACSVGRKKVI
29905	60273	A	30088	1	3639	
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV FADCLAWTCRHKLDLDDISDVA KITGLTSKAIRFYEEKGLVTPPM RSENGYRTYTQQHLNELTLLRQ ARQVGFNLEESGELVNLFNDPQ RHSADVKKRRTLEKVAEIERHIE ELQSMRDQLLALANACPGDDS ADCPHLENLSCCHHRAGKYVG LIRRVKRRIRHRCWPIKTLSQRA VSEFQRLIQPNHQYQSYTRQCA PETDNHADNSYNAGLFIVNSLY TAEGVMDKHSWQRYVPLMR HEALRLQVRLPASVELDDLQA GGIGLLNAVERYDALQGTAFTT YAVQIRIRGAMLD
29907	60275	A	30090	1	699	
29908	60276	A	30091	430	660	HQTHFIVEHRRIMQRTARQNI RHYQIQLSAVQIRGAMLDLRL SRDWVPRSIRRNAREVAQAIGQ MSLPMLQVALS
29909	60277	B	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDDLRTFVAVA DLNTFAAAAAAVCRTQSAVSQ QMQRLEQPLGKNCSLVTVATN C*LNMAFNFLVTPGKSCVLMM RSCIQPNSD
29911	60279	A	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPWSYSRCIRILIAPSSS*Q TEAKPFASRASRTSDDCQWANI SSVMPVKPNSTTPSILRRFSTPK CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	A	30097	87	760	
29915	60283	A	30098	1	2793	
29916	60284	A	30099	308	485	KSLNAICYRNTRTSMACY*PA* VRWPKHSAGLMTISPVLHVISP RHWRLCATRVGRLG
29917	60285	A	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	A	30103	1447	1773	QFAFTEHHQTQEHHHQRSYDC PQRDPRHIDAQVSDQRPCPDSG LREPLHCAQPDSSG*ADNSADH IRRNGGDGAFQKRNRNLTDPH KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	

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29888	60256	A	30071	498	1155	KQPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQRVRIYLLR YGILDWSPTYLKEVKHFALDKS SWAYFLYEYAGIPGTLLCGWM SDKVFRGNRGATGVFFMTLVTI ATIVYWMNPAGNPTVDMICMI VIGFLIYGPVMLIGLHALELAPK KAAGTAAGFTGLFGYLGGSSVA ASAIVGTYVDFFGWDVGFMLS HELWESEFTKLKYEYNNSCPAS VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRESFDDPKSDRAK DFLAKILH*SLWRA YPIARHLTL YRFAPRICYILALPLSQRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKTLRNVLRMLTLLNRTDIPVA GGRGKTVNA
29890	60258	B	30073	861	935	
29891	60259	A	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSASSCSGRNRYPGS*PS RPDCQRSCSHKHAGYG
29893	60261	A	30076	3	227	GGEGRASCSADTGWLPSDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATES GPAEGVIPPQ
29894	60262	A	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	A	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPSRLYAHAH GDTPQRLRLNGRQALSP*FCCN HRAALQRHQPVRLPARQSRQ MRRCNLLYQKASAQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRFQCHRP HGLPGTGPPRH ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	A	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	A	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPAHRRNGPDV PS

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29862	60230	A	30045	1	2142	
29863	60231	A	30046	1	2463	
29864	60232	A	30047	1	1066	
29865	60233	B	30048	790	820	
29866	60234	A	30049	3	126	
29867	60235	A	30050	1853	2257	
29868	60236	A	30051	90	411	
29869	60237	A	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	A	30054	1	1986	
29872	60240	A	30055	339	596	PPYKRRKRRRESVSDGMRNTG KTRRTR*IINLLGRS*NRNFVSV PSGQNY*ISLDHGRENYYGGYS TIQNRLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	A	30057	42	665	KYGV\NPGPYGGTTRKLYEKK LLKLREQGTESRSSTPLPTISSA ENTRQNGSSDSRDYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETEWTS GSSKGGPLQALTRESTRGSRRT PRKRVETSEHFRIDGPVISESTPI AETIMASSNESLVVNRVTGNFK HASPILPITEFSDIPRRAPKKPLT RAEVG
29875	60243	A	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	A	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	A	30065	900	999	
29883	60251	A	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	A	30068	1	2229	
29886	60254	A	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSRCFWWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALLTIVTT QATGRLRARQRKTATPRTIRPG ESTSSSPRSSGSLAPACSVPWM

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29851	60219	A	30034	1	1593	
29852	60220	A	30035	107	195	
29853	60221	A	30036	1480	1605	TILRITFQFCRSNRRRQRQ*NRF STSQRRCYFLLNGEDVTLP
29854	60222	A	30037	1	373	MPSYFTSRIA AVHVSALREEQA HHESKHESFIAQRMFRMFYQ ARNLLHAGQENLFSGLTALTAE FTVGEEATRGKTTGKRGSPDG RILRTTKTRNPRGYMQGRYLES QRDVEATDKPFEFFMNRFRLL AA PRVEFIA Y TGLCEDVIRPQL DEAIAQGYLTECADYWQITEH GKLFLNSLLELFLADGYHMWR MIGAGAH LAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPLGIEQ LPALKA FDTVFSMGVLYHRRSP LEHLWQLKDQLVNEGELVLET LVIDGDENTVLVPGDRYAQMR NVYFIPSALALKNWLLKCGFV DIRIADVSVTTTEEQRRTWMV TESLADFLDPHDPGKTVEGYPA PKRAVSDCAQAVKMTNMISYQ GLVRTFLSTSPNNWL VFMQNG QEVVIDSGKSVS*RSVCFGCFIK HGICSMRDKKISFLV*RRLLNS LSAKKLHGAKQRAKGDLP RMG AFCVPPKRVIRVVICKEGIWKA SVMSKPQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCP PRSRQRRRSGPLPEPAPRVS*Q IFPSQY WRYRQSTENQKQRLDP RGQIVNVPARRIIRQKRKCKV AGSA
29856	60224	A	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	1	1377	
29859	60227	A	30042	2268	2684	RCRRCKRRLRRFRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*QRC SSDGRKITSVHRGRNADGRELT HQA VRL LAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL RHTPAV
29860	60228	A	30043	1130	1310	RLDKQNRQ GKQRQNNGVFHQ QPQRR*RTDVIQMPHSHRHA QRRDHQQLGQH HAGRNFE
29861	60229	A	30044	395	689	VAASVSSMSCAPVLM TVVTR CTLLILSQFMRRKA IKK/LSGSL LPASEVKVLKRDGDYSE/VQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW

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29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK SESDIHLAEHHKQVLYDGKLAS SIAFTYNAKATDAQLCLESSPK ENASIFVHSPHALMLQILTEQV CTQVVHKPHPEPDSTVKIQNPS EQMAVLYCIVLVGGFDLEMN FIIQDAESITCMTLEHCDVTC QAEIWSMFTAILRKSVRNQTS TEVGLIEQCDNLKTCHTSHGSV MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKP DGL SIVSLAKIDWIIERYQLPQSYQR MPD FRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	
29834	60202	A	30017	2033	4226	
29835	60203	B	30018	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	B	30024	1	2299	
29842	60210	A	30025	2	488	
29843	60211	A	30026	1	127	
29844	60212	A	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSLLRICSGVSPRS IPRWFTSVSLPSSFIRIRITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSLV/VGSRPSGLRAFSSD CSPLPRTCSSLRRRVLMITTSRS *SLTYGVDPSVRPVLAASEYF SRRYAGFQNPNNLLVSG*YQG NYRHFILRGYPG/TLKNSNFQL TRSARISLSSRSICTSTGGNTTL PPSSPPDC
29848	60216	A	30031	1818	1991	SPSHIRRTAPNGLRH YQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW
29849	60217	A	30032	2	501	
29850	60218	A	30033	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPQGC DPHMESLI

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29829	60197	A	30012	1	6552	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQIRLGDP GSSRLSMEHGLRSIPAWTLDKFI EDYLLPDTTFGADVKSANVNVV CDFLKERC
29830	60198	A	30013	1	2679	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALK SFAGKEVVFYRPEEDAGDEKG YESFPWFIKRAHSPSRGLYSVHI NPYLIPFFIGLQNRFTQFRLSET KEITNPYAMRLYESLCQYRKPD GSGIVSLKIDWIIERYQLPKVPS PEARKITRRWRI\VKQRI*LGFL RLSEMPRKQGDYRTRIWKFE GLSNVLVIQLNKLIIICVMCLVR DCDVLKTYFHR
29831	60199	A	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIK AHSPSRGL\YSGHINPYLIPFFIG LQNRFTHF\RFMEQKKSPSNRFT QVRLSETKEITNPYAMRLYESL CQYRKPDGSSIVSLKIDWIIERY QLPQSYQRMDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIVFSFRDITSMTTG

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29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERK\NSPRIVQSNDPFEA AYSLSRDQKRMLYLFAQIRKS DGTLEHGDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLYSVHINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIIERYQLPQSYQRMPDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTTHIVFSFRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	A	30007	1	2331	
29825	60193	A	30008	1	1857	MPLRFSSSSRIPYYVNLHKA TGFERIDYNFETHSSLEIATDAL TISDHHPCESAANAETRPSTVL EELARAIRQEKEIKGIQIGKEEV KLSLFADDMIMYLENPKDSSRK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTQPFYN SCENKIKYLAIYLTKEKDLYK RNYKTLLKEITDDTNKWKHIPC SWIVKVAGVESWIHHTQVEVW TPPEETAGSTAHSQDQPDQPR YTCEPLEDLHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGSVMAETA VINHKKRK NSPRIVQSNDLTEAAAYSLSRDL KRMLYLFDVHIRKSDGTLEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLI\PFFIGLQ\NRF TQFRLSETKIPVIIQEAGLSQSEK QAADGIQGVAFPAFQVCDGCG SSLQHFFLLMLVDFQLPPLLNL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HPAISDVLWVCALSHSLEFHRA SDVRADLSNAYSEEVKFGFLL WGLDCASLHRSDFITSSETKYH
29826	60194	A	30009	1	944	
29827	60195	A	30010	1912	1915	
29828	60196	A	30011	1503	1961	

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29819	60187	A	30002	1	1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKKRTTLAPNTQT ASPRALADSLMQLARQVSRLES GHQAPCMKSNNALIVILGTVT DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDFRGRPVLASLLG ATIDYAIMATTPVLWIYPLCDN LKTCHTSHGVSMAETA VINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQND*RRPVL LASLLGATIDYAIMATTPVLWI YPLCDNLKTCHTSHGVSMAET AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMQSPYTDYSGKHGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN
29820	60188	A	30003	1	1653	
29821	60189	A	30004	1	1128	PWISAPVPVDVVEGAMDSVT LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRERTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGVSMAETA VINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEH GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYK\SL CQYRAFVNGGGEKARGKPIL CRYGVGM



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29810	60178	A	29993	1	936	MWLVTTELESTDEHFYHHSK CYWPRAHLGECILSIEAACQAA GGEAGNGGSAVTKATLGSRQG AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST DSSKKLSELCDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPFQRALYS CTICNP*ILIPFSFVIGLQNRFTQF RLSETKEITNPYALRLYQSLC
29811	60179	A	29994	1	1641	
29812	60180	A	29995	1	1551	
29813	60181	B	29996	90	1515	
29814	60182	A	29997	452	1523	
29815	60183	B	29998	9	2021	
29816	60184	A	29999	1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSSNCAPRGISPQELTVDLQTKC DNLKTCHTSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESFPWFIKR AHSPASRGLYSVHINPYLNSLFY GVQNRFTQFRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWVPDLHIHAEDTLLPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE

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29800	60168	A	29983	3	678	GSVMAETAVINHHKKRKNSPRI VQSN DLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR YSFPPDYFHGLALNVC GFSRYT VQDVGGSIILGSGGQWLSSHSS SRQCP
29801	60169	A	29984	2	660	
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV K*HGIEMKCEELIL
29803	60171	A	29986	1	643	
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSN DLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRK\PDGSGIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSVKR GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGSVMAETAVINHHK RKNSPRIVQSNDLTEAAYSLSR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIE/ RYQLPKVPSPEARKITRRWRIV KQRI*LGFLRLSEMPRKQGDY RTRIWKFEGLSNVLVIQLNKLI ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIK AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSQND*RR GI
29794	60162	B	29977	1	1317	
29795	60163	B	29978	78	215	
29796	60164	C	29979	225	422	
29797	60165	A	29980	1	368	MAETAVINHHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGD/EKGY ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETAVINHHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEKDAGDEKGY ESFPWFIKHSTNITSLSLWFFSS CTH
29799	60167	A	29982	1	814	

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29780	60148	A	29963	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPV NVSKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDE GNYTSGDNHTLRDPHYVEDK GHKYLVEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQ KLQQSARKDAELANGALGII ELNNDYTLK KVMKPLITSNT CDNLKTCHTSH GSVMAETA VINHKKRKNSPRIV QSN DLTEAAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICE IHVAKYAEIFGLTSAEASKD IRQALKSFAGKEVVFYRPE/ EDAGDEKGYESFPWFIKRAH SPSRRLYSVHINPYLIPLLYR VPNRVTQFRLSETK/EITHPY AMPLYESLCQYS
29781	60149	A	29964	1	1557	
29782	60150	A	29965	1	2259	
29783	60151	A	29966	1	1959	
29784	60152	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29972	1	1446	
29790	60158	A	29973	1	1191	
29791	60159	A	29974	22	1893	

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29773	60141	A	29956	1	726	MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLLTGQQTP AFGRRVSGVIECDNLKTCHTSH GSVMAETAVINHKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFP\WFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRL
29774	60142	A	29957	1	771	
29775	60143	A	29958	1	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPHMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIPTPAELFDY TSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGNSVLRK
29777	60145	A	29960	1	1731	
29778	60146	B	29961	1	3345	
29779	60147	A	29962	1	1959	

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29752	60120	A	29935	222	527	LPSKLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFHLALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPDIEG DLIQGQRHRDHIGP
29753	60121	A	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLNDAINGGD AESAGLTPPELWPRHHGHGPA GVKLVEQLCQRLRVPNEIRDLA RLVAEFHDLIHTFPMNPKTIV KLFDSIDA WRKPQRVEQLALTS EADVGRGTGFESADYPQGRWL REAW EVAQSVPTKAVVEAGFK GVEIREELTRRRIA AVASWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRSAAVS NHQHFRACGHIDRRRTVQTLA HLTFRFGDKGVTRPEDFVHFW HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAWYDVAIGIPGPFAGRS\ CVILLGDAVREVTRVSNAPPAK RYIGGSPRRGFINSNMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	B	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSSLLSLRAFW ASAPVTATNPPDTLNGGFFRHD HKSSCMTRVPQVRSPTLNRSQ GASRPRGVIQQLGHRDPNGDDS HRVRIGLIKHP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	A	29947	1	966	
29765	60133	A	29948	1	675	
29766	60134	A	29949	1	792	
29767	60135	A	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	A	29955	1	606	

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29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSYYV AESGLVTTVGKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVYRPWGKY DSIDAGDRYQVKRITVKPGEGL SVQMHHHRAEHVWVVAGTAK VTIDGDIKLLGENESIYIPLGAT HCLENPGKIPLDLIEVRSGSYLE EDDVVRFADRYGRGNDMCKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLPKPTIVLGGDVR LTSETLKLALAKGLQDAGVDV LDIGMSGTEIYFATFHLGVDG GIEVTASHNPMDYNGMKLVRE GARPISGDTGLRDVQRLAEAND FPPVDETKRGYQQINLRDAYV DHLFGYINVKNLTPLKLVINS NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	A	29921	426	1861	
29739	60107	A	29922	863	1388	EPERTSIKSSGIFPGFSRQCVAPS GI*MDVVFTKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGD AFHLVAVARVDRVIFAPR TIHFAMHPMLMATIGFDLLDHF FHILYRVTVGNQHRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVGADLP
29740	60108	A	29923	1	2055	
29741	60109	A	29924	1	2047	
29742	60110	A	29925	1	1294	
29743	60111	A	29926	1	1020	
29744	60112	A	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	A	29929	210	340	YGDVEHESWLSCVRHAH\PRIP FA*PTLISLQKRLGKWSGVTGA
29747	60115	A	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHHYRNLP/VPNGPPLSLL P*YCKAKFKPSTSQVP
29748	60116	A	29931	63	281	
29749	60117	A	29932	345	467	LPTRCTYTNLRRRSPPAWYY* *YWHRDICRSTPARRQTE
29750	60118	A	29933	29	281	MFGKELGRRDVSQLGAAEITYI LKD*T*ES*EILCGGRFLLPLRG RTLGGGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR
29751	60119	A	29934	520	714	

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29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL VFLLTVRSLSCRSVGV CWRSTR DLVCLGISSGGCRTL NIAEQQM LLPDCSSGIFVSEGY LAV*GVSL PLLGGASQLGLGSMAIFMILILP IHEHGMFFNLFVSSFILLSSCL
29725	60093	B	29908	168	863	
29726	60094	A	29909	340	612	
29727	60095	A	29910	1	834	
29728	60096	A	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	A	29913	1	1278	
29731	60099	B	29914	1	2007	
29732	60100	A	29915	406	615	
29733	60101	A	29916	52	391	SNRLCLKMHSSRSSCVMFFSSIR SFKDFSLVFDDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVG CWRSTDPVCLGVSSRGCQTV NIAEQMMLLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLSEWQSGQ SPAGAAIAAFDNR
29735	60103	A	29918	84	3661	



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29711	60079	A	29894	1	1890	MYSRFDIVVAEPICTLTTFGKET VVSQSQTRTTTTDDPLQVLQV LDRADIRPTHNEDLPFQGGALG LFGYDLGRRFESLPDIAEQDIVL PDMAVGIIYDWALIVDHQRHTV SLLSHNDVNARRAWLESQQFSP QEDFTLTSDWQSNMTREQYGE KFRQVQEYLHSGDCYQVNLAQ RFHATYSGDECQAFLQLNHGN RAPFSAFLRLEQGAILKLSPERFI LCDNSEIQTPIKGTLPRLPDPQ EDSKQAVKLANSADRAENLM IVDLMRNDIGRVA VAGSVKVP ELFVVEPFPAVHHL\TITAQLPE QLHASDLLRAAFPGGSITGAPK VRAMEIIDELEPQRRNA WCG/SI GYLSFCGNMDTSITIRTLTAING QIFCSAGGGIVADSQEEAEYQE TFDKVNRILKQLENYRRALRDL KEEVAIRLSPFELSAFCSPSIASM ATRYPNGRHIPDLRLPKERGIH VFTGNGKGKTTAAFGTATRAV GHGKKVGVVQFIKGTWPNGER NLLEPHGVEFQVMATGFTWDT QNRESDTAACREVVQHAKRM LADSSLDMLLDELTYMVAID YLPLEE VVQALNERPHQQTVIIT GRGCHRDILELADTVSELRPVK HAFDAGVKAQIGIDY
29712	60080	A	29895	159	475	VKVNLPWAMLLHSGYADHPYS RFDIVVAEPICTLTDD/GRCSHIS LYAAGIINSDSKGAVIMPPIGA AIRLITSEPAVPVPHRIGSRPAITA TVIAFGRTTRTAP
29713	60081	B	29896	158	810	
29714	60082	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGAPRSS RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	C	29906	1	1587	

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29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK GSPCFGPGGGLIN*AAADIPVAS DNPAHYADAIRYNARTPLQAG VYFVRDGGPGPLASVRNKERYF ANNYIYDMGRNKDGRQSTWY MGLGTDIDTGLPMSLSMNVYA KYQWQNYGAANENEWDGYRF KIKYFVPITDLWGGQLSYIGFTN FDWGSDDLGDGSGNAINGIKTRT NNSIASSHILALNYDHWHSV ARYWHDGGQWNDDELNFGN GNFNVRSTARGWLPGTICRPDK MRQHRIRHCAPIAGCGTGCRPD KTRQASHQAQMSNAYDYSEIQ PPSEGEILLDAQPLESWSSKAFA RKVAYLPQQLPPAEGMTVREL VAIGRYPWHGALALLGAADRE KVEEAISLVGLKPLAHLVDSL SGGEPGVDRMLVAQDSRCLLL DEPTSALDIAHQVDVLSLVHRL SQERGLTVIAVLHDINMAARYC DYLVALRGGEMIAQGTAEIM RGETLEMIYGIPMGILPHPAGA APMNTAHHAAIDPNRIVALEW LPVELLLALGIVPYGVADTINY RLWVSEPPLPDSVIDVGLRTEP NLELLTEMKPSFMVWSAGYGP SPEMLARIAPGRGFNFVSRNTP LARTLQLJLREGPRGHPALVQV VDLLIEPPQLPLLVPSVQTRIPRI QPQSHPAHGVNEAVRNPTVWV APFIDEIISIIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	A	29893	255	1360	

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29691	60059	A	29874	463	889	FFGLVTSSPSADSPAMLDTRNV SHTGLGPIIPLTFEAGIHTRPTPN SPPRSCLAPAICA*FFSPAARITT CCASLYRSPLKTLRSVRFWRSS ASVLMRRSSSAAPMPEATLRVL SGLRGSRSDKAFTPHPTI*CLEA FPGSRAFVASAP*CLTLRANQR KGCW
29692	60060	A	29875	524	1006	SLLAWLSGINIFASSRIAIASPLA ASVPLSMDNISLCTPSGVPEKV TSTVLTSVPQSCKLMMKDFSGP *FP*EKRVSETSPNCTLICLLSCA STHVLRRNDPLMLTVPSWANS SQPHVNPKNRIQIIPFNITPSLV NQIKIETTRAFTPLLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	A	29877	1	470	MQRRDGDIALIYRSKIGPRTSIT FTARRANPVQRIAARILLRDHLI CRMSTAAARHANTFDLIQSGG ADNFAAIYGGANDRITRADA/V SRGCWKLAPVRDIKRTVAAF YHQDIQPGSCHDQNAL*STGFW REQSGGQ*P*AG*TNSRTRCCIT GR
29695	60063	A	29878	734	1306	
29696	60064	A	29879	743	901	
29697	60065	A	29880	771	1013	RLGTVGTDLSWCYQYQLCYQ* ALPFSTLPAKLNGCQRRRCA GTHSLWHADLGSVWPDADSLF QRDGRAGGGATRLLRR
29698	60066	A	29881	1094	1345	
29699	60067	A	29882	2	751	
29700	60068	A	29883	239	483	PTPQHLYHALTGSTIMSQRGV DIPCHWHDITCGHAHSLPHRRG RKA*SMGNR*YSCTWCYCEGG TEKAIWPGDGCPLSV
29701	60069	B	29884	228	803	
29702	60070	A	29885	488	636	
29703	60071	A	29886	1	2117	
29704	60072	A	29887	665	795	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29666	60034	A	29849	102	296	YRNSHNLLQGWOIHRGDLLYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	A	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRIHH
29670	60038	A	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	A	29855	1591	3150	
29673	60041	A	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HSLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLSFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	A	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTSIGHVLGSCCW NGKTLRKSDSRWQQLLRSLIR R
29676	60044	A	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCIMAIRSPIRMASRR SWEIKTMVR
29678	60046	A	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	A	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRRFR*RQD CQTSVFLLRPVANRAPA
29683	60051	A	29866	1	715	
29684	60052	A	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAAALTSGVAHLSSS GTPFRPFCLPSC*LSSSRAAAIST CSLYAAWFPLTLIRCRGIRKSPII CGISRCRCWRQ
29687	60055	A	29870	1	439	
29688	60056	A	29871	14	106	
29689	60057	A	29872	2518	3024	
29690	60058	A	29873	448	537	

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29653	60021	A	29836	3	2037	CTSSPDPPSGLPPGFAKLTSIVT LVEVGVSPEPDEGWLYLAVVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGLTRSIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLKLPGIHVREESR RYYPSPGEVTAHLIGFTNVDSQG IEGVEKSFDKWLTGQPGERIVR KDRYGRVIEDISSTDSQAAHNL ALSIDERLQALVYRELNNAVAF NKAESGS AVLVDVNTGEVLAM ANSPSYNPNLSGTPKEAMRN RTITDVFEFGSTVKPMVVM TAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERRCKTTINLVPENEVLNV LEGEDAETNALRAKRRCPKCG TAMDSYLIDPKRKLHVCGNP TCDGYEIEEGEFRIKGYDGPIVE CEKCGSEMHLKMGRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVPLPELPCEKSDAYFVLRD GA AVAARFNDDRHRRLAVLY ADQADLYGVADSVSAGDSL SA LYKHERRLVVPLLVS SLLFLY RHGIRLPCGPSGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ* AIVQLPVCGI* PRSD SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI* TERHCRSGNP
29654	60022	A	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRK MPLSSDLGSL HGLAGNHSPICARTPHVATVL RQLELEDKHWNGSG* FARLG WKPQSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	A	29840	3	86	
29658	60026	A	29841	1	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK* VGGSSRVNVPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	A	29844	115	903	
29662	60030	A	29845	1194	2311	
29663	60031	A	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVYPLCYLRQLAVQANPRR MRCIARHFNNGNRHLTTTINFI *SMVSLIANRLLIIDLIHTVDFY
29665	60033	A	29848	1	228	

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29648	60016	A	29831	202	918	AVDTGLADHRDRTEHGGFAAA IVHRIVKHFITAWAICQQRNHA ALVVIRLRLEANHRRHRTGRG\S VDRVSAARSLSSGTMPEGVW RIGVFTQLSVA/WHQ*VDLLIVF QFVRDTTDDHDVGIFALAAND RAAFDNILDPTGSVDVLLPLPG RHNIALALAAAALSMSVGATL DAIKAGLANLKAVPGRLPFIQL AENQLLLDDSFLVNAAQQNLS VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRAVP*RC/GR QLVSSDNISNDPMNVIDWINMY ALAVSEENAAGGRVVTAPTNG ACGIIPAVLAYYDKFRPVRNER SIARYFLAAGAIGALYKMNASI SGAEVGCQGEIGVACSMMAAG LTELGGSPAQNMEGKIDRPEE YADIATKCVTNFREKNRDRCL VILSRNDEALNSQRTSEELHHY YEIVWDEEQTHKFKNISPHLQRI KAFKTLGGPHGNITVDMVISAQ ELLQEDMATFDGHIVEALMKM PEVNAMYPELKLHAIGWVKHK CIPGAKWPEIQAEMRIWKKRRE GERKETGKYTSVVDLARARAN QQYTENSTGKISPVIAAIHREYK QTWKTLDDelayGRCFADRQN LMVCLRSMPNVFTGSCARMRC CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA MIPNFWAFLGVTTWIFMAAG GAESVA\CTLTTSKAVRNRSFK* SS <sup>5</sup> PGILSGYVSRSSGSPISLISP ASLCAGHMRFFCSSSKPTCSNP RTFAAALSSAWSSPSPNEGFSSN PAFLGTSLMMFHLERRCIPIV TTDLLPLTSGDVGVLVLLCVGLD GSLWSDCRMTESVSTTNTPTPIIT SRNS
29652	60020	B	29835	46	893	

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29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA SVVSRDGFVIAGGGGMVVVEE LEHALARGAHYAEIVGYGATS DGADMVAPSGEGAVRCMKMA MHGVDTPIDYLNHGTSTPVGD VKELAAIREVFQDKSPAISATK AMTGHSLSGAAGVQEAISLLM LEHGFIAPSNIEELDEQAAGLNI VTETTDRELTTVMSNSFGFGG TNATLVMRKLMIASASTSILR
29633	60001	A	29816	1	2472	
29634	60002	A	29817	1	469	LFNREVCCLGQGS*QMAL*LL GIESYIT*L*SGGDNASIGVIPDP AAIAR*RPWRSACG**PKCPLA DVFAGHSGRKRPPSMAFTATLI SPGTGRRAINSVLAQFKAGESNI WLSALPTPLTPTIRITNGALPSTF SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	
29636	60004	A	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK EMGFDGFEIDGKLLVNNIEEVK AAIKETGLPVTACGGYDGGWIG DFIEERRNLNGLKQIERILEALAE VGGKGIVVPAAWGMFTFRLPP MTSPRSLDGDGRKMVSDSLRVL EQVAARTGTVVYLEPLNRYQD HMINTLADARRYIVENDLKHV QIIGDFYHMNIEEDNLAQALHD NRDLLGHVHIADNHRYQPGSG TLDFHALFEQLRADNYQGYVV YEGRIRAEDPAQAYRDSLAWL RAGQVADKVHASYYCTRNDLE LVAVCDSRLSQAQALAEKYGN ASVWDDPQAMLLAVKP*FVGL VIGAGQVADKVHASYYCTRND LELVAVCDSRLSQAQALAEKY GNASVWDDPQAMLLAVKPDV
29639	60007	B	29822	96	821	
29640	60008	A	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	A	29825	1	849	
29643	60011	A	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	B	29829	1	1812	
29647	60015	A	29830	685	1146	

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29613	59981	A	29796	1	738	MQPWALPTVGELWVCGRPGA ALRAGTEPSSRALGVSETALPA EIKLRVIRVGHSSPLAQLASFQK PVLFLVRLNSRRFLFLSLARSED GILFAKSKHSSPLSLTPLRCIVL MRMYEQLMSGDLCQRMMPMS RNNPGYWNPQ**SEIFKGSPAQ TMATLTCSFKKPPKIPYKAIAL ATVFLIGAFLLIIRLPSCCQGYI KQRGGRPGPFQLLIHSHWCSY PGFYPPAHRFTMHPKGLPWVN PNE
29614	59982	A	29797	1	186	DCRLRAGDPRRSHCAVSPTGGS RALSGYRY*SVDQPRNDGVDQ *ATLRASAHLQTA VVEFSA
29615	59983	A	29798	724	1015	RSHPQCGYLQNHTSSASFSAPA RKG*NRHYAFARNDR LVPAPCS HHHQ*PAFPAPVHLH*PVDLST AIDAPAVNGDGKARPSKRRYQ RLSVPEVVQY
29616	59984	B	29799	1	4182	
29617	59985	B	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	A	29802	1541	1852	FALFANRVSLAANVSGRGSPC WRRRIAVVCCSTNR/RSALDIA HQVDVLSLVHRLSQERGLTVIA VLHDINMAARYCDYLAPCAA VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRLFTTAND QPHRPARRIISIAGIKWRYSDFLI NYCAGRAVF*RETGSVVERWH HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASARYVRATLSCSR NSTLRWKK*RKMALTKPSTTN GSRSNS**MNFFL*QAPPG*PSA LPFVH
29625	59993	A	29808	3	116	
29626	59994	A	29809	1	1469	
29627	59995	A	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQRA CSGR*VPLRLPEVQSTDRLLS QRRRVSPDRQWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	



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29595	59963	B	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFHCPVTTNDP HFMKWRAAAHGGENIAFKLAN LPFFGDIRESHYQVVINRADRG FNPDDFTGARQQQKFVLIAGGF P*QLL*TNAVIGREFRNVQECIG LHTAGFANAVTKHF/W*M/PRL HCTIWRSGSRTITGRSRWSTAI NCRVCSFCAISTLASRTSAR
29597	59965	A	29780	938	1250	PGRVSGKADGSV/LAGNLLPG FFCPLRLRGKYQPEV/IASITRRR YQLLFLAVASHQATAAGCGVN ALSDLRLCSVCRPDKTHSVASG NGCRMALPSSPFSVIL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT RPWASDIKAQCAGGISRFATGN GFKRLCDTLRYLQAIENGLKN WRLIHIA TVRRCFPPT/LSPATID AINVIGQWLAQDDFSGEVPYQ ADCVILAGNAVMPPTIDAACKIA RDQQILAEGDFGLRCEIRDWCA NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVVLVHHFH AITHIRQSQITRYIKLLRHRH TQRRFTACRLRVDAPFGNHQC CALHCLRKIDRIQHNFNARFNIR IEKYRRRNTHARSAA/DPPSGR H*FQFAVVKHGRNFAAPVQVL RPSALPLFAGQTPPPRRVPLPA GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/ HVPFSHESV/WENIVMTRQAQG ANFT*TLFCFGIGFAVIA*NCAI DPDISIRFFSKEETAT/GDRPDQI AAHLWRFPPTGGRFVHHRGAY AAHIFRP*YLNGRSMAEQSMILV TGELLVELNLEPSQVGNFAEK YYGPASQVV
29602	59970	A	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1	194	
29609	59977	B	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	

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29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPVYT**PTA QGLSARQGCTKGHQVRRYGFR HD
29573	59941	A	29755	66	372	
29574	59942	A	29756	1	992	
29575	59943	A	29757	1	393	
29576	59944	A	29758	1	3753	
29577	59945	A	29759	1	1098	
29578	59946	A	29760	320	703	
29579	59947	A	29761	2	673	AAFLRECKDPQTMVPKAINSVI WRIGLFYVGSV-VLLVMLLPWS AYQAGQSPFVTFFSKLGVPIYIG SIMNIVVLTAAALSSLNSGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVVYVVGVF LNYLVPSRVFEIVLNFAASLGIIAS WAFIIVCQMRLRKAIKEGKAAD AHFTPYHATPLRNVMLHIYVLN GVSFRFSVIDTNQIAQRCNRFAL LCGA
29580	59948	B	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLIGIVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVSIGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRIPISARLQR*AGSFFS FLGETGSLSCGLSLSFKSCCEAK NCSGSRGSSP/G*IPGVQEWNI FSRF/HGVGLASLRKQRAPGDQ SPTGLLGE*AHGEIPVGNRSG KTRA/RGGPRGLEVSWSGSLTH SRG*ASLTSSHNSCHIRRGHPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	A	29767	362	1850	
29586	59954	A	29768	1	1401	
29587	59955	A	29770	1366	1515	YDQAELDQLIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	A	29771	1	1827	
29589	59957	A	29772	419	1295	
29590	59958	A	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	A	29775	345	652	
29593	59961	A	29776	596	2297	
29594	59962	A	29777	184	283	

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29562	59930	A	29744	1	2352	MLPDSSVRLNKYISESGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVPFPIGRDLKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPIITEEFIRGMSAG VPILGTVTKKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDDELIDLFKLIENSSEVKP KRRPNRKQRASNVSQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHIFWLSLGGLLL AAEMLGGNGYLLWSGVAAVIT GLVVWLVPVGWEWQGVMAFI LTLAAWLWWKWLRRVREQ KHSDSHLNQRGQQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQQLVAHGLQLL NVSFDLRHLFQGRLEFGCALR LLTDSQSRLSRKPRGWRGLYG YSPPCGDIVRYHHHDLVATLH VHINHDDCLEIAVLKGDMDGV QHFADDVIAQRGFFFAFSYEDT VIKIEKDFTMSGKPAARQGDM TQYGGSIQGSAGVRIGAPTGV ACSVCPGGVTSGHPVNPLLGA KVLPGETDIALPGPLPFILSRTYS SYRTKTPAPVGS LGPGWKMPA DIRLQLRDNTLILSDNGGRSLYF
29563	59931	A	29745	1	3075	
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCPWEKVTLFSLQWS AYRQANTSGLRHSASSLLPLAC RY*R*WRWQKLA AVLASARQ SVKSLAYCWQRFVTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569	59937	A	29751	1	474	
29570	59938	A	29752	137	586	KTKTNIKL*AAPITRMVMVRHA VPHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHA VDTINRGEIHIVEPDLA SVVKTA VEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSIAPVLKKGAL
29571	59939	A	29753	2	557	

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29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTV DHLQ ISQCPYIPYPNFPDTS PGTPG LL QPPEGHAYDAYWRCVRAVRG QRVSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YGS G VRSWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTCSMTACPCTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPRKQQASGWLWACP RIFLVIPHSSHPAARRTNGSVGG SNRNR FVIITGPGPQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGSVSAPTIQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPPRQSRRQFPRLSPL DAHQRMGDVSIQAVKEARTC

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29547	59915	A	29729	1	817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRSYQ VANGIAVLPVSGTLVSKTRALQ PYSGMTGYNGIARLQQAISDP GVDGILLDMPTPGGMVSGAFD CADIARMRDIKPIWALANDMN CSAGQLIASSASRRLVTQTART GSIGVMMMAHSNYGAALKTNGV EVTLIYSGDRKV\DGPNPYEKLPI KDVRADFQTRIDATRISAYTGM SVQDV/LDTEAAVFSGQESWDN GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	A	29731	215	871	
29550	59918	A	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDGAGRFCSLAKETVTPQW *GVLTSIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLLGYSLVCSRVLAC FWPGSDFWPRSRRKTSHTLVEA FPV/VVIFVSWRNPQVAPSAH QNRPSRNPVSRPPNTQRVARRK HYALADGY
29553	59921	A	29735	403	588	
29554	59922	A	29736	1	743	
29555	59923	A	29737	5	97	
29556	59924	A	29738	756	935	
29557	59925	A	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	A	29741	1	2718	
29560	59928	A	29742	3	357	

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29541	59909	A	29723	1244	3261	KTINRTSLWYWTLHDHWSVTG RCAFTDVTKVEDHHEPQTQTR GLVMTTS*ATT*KLTVSLTTAC VMNWV*MQVIPSP TAKIRL*LR TSNWL TSTTTLT/NNDVNGDSI DNGTEGSAVRVGLGTQFSFTK NFSAYTDANYLG GGDVDQDW SANDLTGITAKDAQMLS VVKP LQEFELFVLAAL ESRGTLADILK AAGATTANITQAIEQMRGGESV NDQGAEDQRQALKKYTIDLTE RAEQGKLDPVIGRDEEIRRTIQV LQRRTKNNPVLIGEPGVGKTAI VEGLAQRIINGEVPEGLKGRRV LALDMGALVAGAKYRGEFEER LKGVLNDLAKQEGNVILFIDEL HTMVGAGKADGAIDAGNMLK PALARGEWHCVGATTLD DIAS TVKRCWTSHQHQTKNRTRRTT TRNIRFPNQMI EQINIALEQKGS GNFSAWVIEACRRRLTTGGPHV MYVLHHADKPNLYHGLPENPE ISETVKFWKGIWKPLAAVGFAA TFAASIFHYERVIFLTGQVEDH MANLIVAQMLFLEAENPEKDIY LYINSPGGVITAGMSIYDTMQFI KPDVSTICMGQAASMGAFLLT AGAKGKRFLPNSRVMIHQPL GGYQGQATDIEIHAREILKVKG RMNELMALHTGQSLEQIERDTE RDRFLSAPEAVEYGLVDSILTH
29542	59910	A	29724	1487	1821	QYRPESVLEDPRRSDHHRRTDS FRETSFIVQSIVCRVSLSRAILQS KRL*EPGEFPPDPSSPEQRWPV CYP PK*SDR*PEYPHSPGRQES QSRYLPAFRHRYSYQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	A	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	A	29728	1	1443	

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29533	59901	A	29715	107	1315	KCADLPVRGLRHCWRRREDPS GADRSFSALIHSGRAAFWPCR* QGALMSIEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSPSQRSYS VLRSKFDAWLMEQAEEGAQL ITGIRVDNLVQRDGVVGV DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVA/VGVKELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNT LSLGLVCGLHHLHDAKKSVPQ MLEDKQHPAVAPLIAGGKLV EYSAHVPEAGINMLPELVQIP CIERNAINAVKAVNAARMAMR RTSAPRVSLDKVIETMYETGKD MNDKYRETSRGGGLAIKV
29534	59902	A	29716	3	264	
29535	59903	B	29717	85	737	
29536	59904	A	29718	171	820	LGVCAMTNSQCG/CDEYRSKN GYEGARKALTGLSPDEIVNQVK DAGLKGRGGAGFSTGLKWSLM PKDESMNIRYLLCNADEMEPGT YKDRLLMEQLPHLLVEGMLISA FALKAYRGYIFLRGEYIEAAVN LRRRAIEATEAGLLGKNIMGTG FDFELFVHTGAGRYICGEETALI NSLEGRANPRSKPPFPATSGA WGKPTCVNNVETLCNVPAI
29537	59905	B	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	29721	285	449	TPAARDAQLSGGRGWY*CSAG NGLMQHRSQSGDWRAGRPFTE GW*PTPDWQIEA
29540	59908	A	29722	411	557	

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29524	59892	A	29706	1	550	MESGVATRPIADFDVYIDKLTE FVYKTNLFMKPIFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILIGRPNVIMRIQKLGLOI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VG DYHEHFSVVKNVFGYRDGV HTAGAMNALLPSGNTFIADTY VNDEPDAAELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTGVPVLMGVAKP VHVLTPIASVRRJVN MVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINAVFFRFNIQAVFV ALRPEVIAIMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTPLWAWLKLLW QRIDEDNM TTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIFANFLPATGDVIQRYIE QFVANSNKMTAVGAGQSGDQF LFALFNCQCFCDADELKRIKNE EPKMGMELNLVQLIAYTDWNE TQQKQPDGSWVNYNDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFGAAGI DSSLRPVW*T*TLRDQMSGGQS AKQPGRFAQWFYP*RLPETG*V PE*CL**CELIRAN/DHFLVSILPL RSPCVPLHLSTTPRLAMDLTG LSGFPIPLSQA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	A	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	C	29713	1	3126	
29532	59900	A	29714	642	825	



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29519	59887	A	29701	1	753	MLALDQREAMRMIFPAVAGAP APALSPYAS/ARILVDQQFCYRQ VVEQNAIAKSCAMIVA ADEFIP GNGIPVDSVVIDRKNPLQIKQD GGKALKLLVLWRSEDAQQRL DMVKEFNELCHSHGLVSIIEPV VRPPRRGDKFDREQAIIDAAKE LGDSGADLYKVEMPLYGKGPQ QELLCASQRLNDHINMPWVILS SGVDEKLFPRAVRVAMTAGAS GFLAGRAVWASVVGLPDNELM LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA PGV*RSEQHESGSGAVSGTGY WCSRDRSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS GAALRRRRRQNQTIAVGWRLA GTAHACNIISIRGYGSEDA/Q/ QRLDMVKEFNELCHSHGLVSII EPVVRPPRRGDKFDREQAIIDA AKELGDSGADLYKVEMPLYGK GPQQELLCASQRLNDHINMPW VILSSGVDEKLFPRAVRVAMTA GASGFLAGRAVWASVVGLPDN ELMLRDVCAPKLQQLGDIVDE MMAKRR
29522	59890	A	29704	370	1080	
29523	59891	A	29705	547	928	RLTKVEMPFYGKGPQQIELLCA SQGLNDHINMPWVILSSGVDEK LFPRAVRVAMTAGASGFLAGR AVWASVVGLPDNELMLRDVC APKLQQLGDIVDEMMAKRRFIP LLRRWVDLALTRWLITVSKP

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29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRLKRLLLSRK TRMP/GFTNPRYGAGAATNPDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHI GFQGTLLIEPKPQEPKHKYDY DAATVYGFLKQFGLEKEIKLNI EANHATLAGHSFHHEIATAIAL GLFGSVDANRGDAQLGWDTD QFPNSVEENALVMEILKAGGF TTGGLNFDKAKVRRQSTDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	C	29688	1	2130	
29507	59875	A	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQVLSAADVRAKLFTLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	A	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	B	29692	1	441	
29511	59879	A	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLASAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITS DIC CPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLEITSPAIIFSPTLHSPA AH HQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMGKEGSS PAKSLAPPLCEQMGGEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSRIPSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	A	29699	353	2776	
29518	59886	A	29700	158	605	PERSGLQEAGGGSRGWGKRSL PPAETAGLSGYMCFRAWLSLSR WDS EDGHWGAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R\*SRIPFTDSV*LVHILLPVGPL AIFFINLAFPGIRESWEQLLILLE KPVGLEACPCKSGKGRP

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29488	59856	A	29670	1	1167	MPWLSTGAAALITALAVVELN DDDDHHHRNNSPLPTPPDDES DDTPVPPTPGGDEIIPDDPDDTP TPPKPVSFNNDVILDKTEKTLTI RDSVFTYTENADGTISLQDSNG RKATINLWQIDEANNTVALEG GNTSACRQALKIPKGSSDYTVT WKGGHFTFYRRWRCKVHKVV FEGSPVTCRYVLNRKNSWHV AHIFRRHAKPEEQ/CSHLFPYPF HHDLDEVLNPDVCLVVVCT HADSHFEYAKRALEAGKNVLV EKPFTPTLAQAKELFALAKSKG LTVTPYQNRFFDSCFLTAKKAI ESGKLGEIVEVESHFYYRPA ETKPGLPQDGAIFYGLGALFTNQ QGFFKSSLLSIFADSSSSVAGRS PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSEPSWAVAPGKAGDPHHS AEWARNSTPSKDQA*RRPHTNIC VTAYQGKVLLVGQSPNAELSA RAKQIAMGVDGANEVYNEIRQ GQPIGLGEASNDTWITTKVRSQ LLTSDLVKSSNVKVTEN
29493	59861	A	29675	720	4525	
29494	59862	A	29676	218	990	
29495	59863	A	29677	54	723	
29496	59864	A	29678	1	2229	
29497	59865	A	29679	2	235	
29498	59866	A	29680	279	1275	
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD CWVDDARLVLANAQMVVRKG GEVLTRTRATSARRENGGKKY SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	
29503	59871	B	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHRQTDGGAVFRVYPGGG PRRECWFSSLDATPGWLLQ/ LYERDRH*PASTG

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29476	59844	A	29658	1	1126	MHEVTLEDPSAAILITVITGHG EIITLKRSSRRQNDIRMYCRRRP EAFRDHHQLRFLPGTDQAIGIL MMSKVG TARPPDKTNIREMSV HTVVLICATRVFQCFNNAGNR DFIHRIAATRQAALHGREHRT PRGVTTIGKMVRKTKTAAGWE HESGFYLDGVVVLNRFKSNVA GKMSSGGAANGSYHSNGLGGH IETGMRFTDGNWNLTYPYASLTG FTADNPEYHLSNGMKS KSVDT RSIYRELGATLSYNMRLGNGM EVEPWLKA AVRKEFVDDNRVK VNSDGNFVNYLSGRRGIYQAG KDLDRFKNLVLVHAARYAADL SYLPLMQELEKRYEGKLRIQTV VSRETAAGSLTG GYRH*LKVG NWKARLACR
29477	59845	A	29659	1	1989	
29478	59846	A	29660	3	159	YKELNLADSSLSEEALIQAMVD IPKLMKRPKVVANGKARIGRPP EQVLAEIVG
29479	59847	A	29661	360	744	
29480	59848	A	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSPPDR TASGAGGGDHQ QYGAGLRQTFCLCQRLSARTC* RLSASVCAT
29482	59850	B	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	A	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

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29468	59836	A	29650	1	1253	MVSVTALKAAFLELFIPPSGLV VSLASGVKLQTFVSVTAHKG SVDPKSDQHGLVVSASGVKL QTFARRAEFPASQQQREVPRHD GGNHADRFTHDHRQLMATGG RHFAlHFVDRFGVPANGARRAG NIITQTVTNRFAGVESFQQCLF GIYAVCERQGAIEPGPYARLFL ATFFIYTSSFKPPLPWLRSLPRN TTPAVVRTAKGQVTAKYVIVA GNAYLGDKVEPELAKRSMPCG TQVITTERLSEDLARSLIPKNYC VEDCNILLDYRLTADNRLLY GGGVVYGARDPDDVERLVVPK LLKTFPQLKGVKIDYRWTGNL QLTLRMPQFGRQDTNIYYMQ GYSGHGVTTGGSSRVGLMAGSQ ISRVSV/CINP*YHRFNLHWRYV ADAISADGAFRTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHYPYCW YPYPADSADISVNKHRRNATQ LHVSCSFLLSDQRFHHEAVPR RVVLFTFNTCVDKYIADIRSRT NGLGFLYAFKQRNSHFVFNAQ RHRHSACLR
29470	59838	A	29652	1164	1273	
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT EEALDQSNADLITLLADWFKDL GFNVEVQVPVPGTRNKFNMLAT RRHEGRYITCMQPLPIIAEQEQE PEMTVRYIISADLTAEKFATA IRNHWHVENKLHWRLDVVMN EDDCKIRRGNAAEFSGIRHIAI NILTNDKVFKAGLRQGWEDIED FGETHLDLQYQYDFENGIPVH DTIARVVSCISPAKFHECFINW MRDCHSSDDKDVIADGKTLRH SYDKST/RRRGAIH/VNNAFSTM HSLVIGQIKTDEKSNEITAIPPELL NMLDIKGIITTDAMGCQKDIA EKIQKQGGDYLFVKGQTQGR L NKAEEKFPLKELNNPEHDSYA ISEKSHGREEIRLHIVCDVPDELI DFTFEWKGLM
29472	59840	A	29654	2	1587	
29473	59841	A	29655	236	666	
29474	59842	A	29656	1	1953	
29475	59843	A	29657	2202	2333	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH CWTTAVACHQCEDAPCANVCP VDAISREHGHI FVEQTRCIGCKS CMLACPFGAMEVVSSRKKARA IKCDLCWHRETGPACVEACPTK ALQCMDVEKVQRHRPRLNFLR LWYVVHAHTLMRMRPRFIQPW EEVVP RHHQHAACFQALIELLG RNGQILKP
29458	59826	A	29639	391	812	HSALCSCRMRRERLIRPTKTCK FNRLQRLCRPDKRSASGNFAVV IRLERVSL LAPFFYGVLLKCL MPKRQCNEADHHQTHTCAGQ KKMATHPLPGENKFIIGEDREY RWALMFPNENAPVCWVGHR *KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	A	29641	1	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS V*GWMFTVP*SPSGRVVF*FCH L*ATCGN*LN*THSLSQGQRAF CILGFLPWHSRRIRSHVGLENEC KVLLSGRSSQMGEP*GR*FSP* VGPLGGRALLQLPQPNSV/YVL PVSGLLVPAGE/CPLNV*PLVCS SANVLLSTSSCFCLCLARVSGF YRHRMGA/SGGFL/M*V*RKGS SFNFLHMA/ASSWDSYSGHHFF *AGADYFFASSVSSLPLVLLHSL HSFF
29465	59833	A	29647	1	1422	
29466	59834	A	29648	1	768	
29467	59835	A	29649	1	885	

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29442	59810	A	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS ICYSHGRDLAPARPAQPPQPRD QPQVRPLCSPHAAAAAAAAAAL TWSCGPPAGFLTAPSAGSRVRL AARQQKAAPRKASAEPDRDKK LAPKLPQNALLVGKGESPRFIPL SVFFSKTFQRTARILKRSASDRL PWVTSRTCPCGGIRTPAEMTRY LRFANLTGGISEVSGFRDESGIN FGSWIAIPPVEKMOVCEGKRSAS CPCFLLTAKFYWILTMMQRTH SQEYAHRSIRVDGD
29443	59811	A	29624	1	2740	
29444	59812	A	29625	1	1614	
29445	59813	A	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	
29449	59817	A	29630	674	867	LDGDGIESINSLGQYGHFHDIDS SYP*AWNENVLFPVCILFYFVE QWFVALLEDVLHVPCKLDS
29450	59818	A	29631	746	1985	
29451	59819	A	29632	1	2211	
29452	59820	A	29633	139	247	KTSAAEKPKWRKEARNARG* KRKRRLMLQRSQVNR
29453	59821	A	29634	335	556	
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA LSPDEFISPVCWLARLVRWRCF FAQKAR*SPAKYGILGELTTGS KLVKANGLMEASTIAAILLSV AGGVLAYWHVLVAWPHAHWP TVSRQQQLMASTLPFTSPLAQ IFPWRAITQRTMRMPFVIDARD ALLQGVFAAVNPSAHLNDSRH RRINKNVIEPGISCQRPQHLDRI AHPFGIHIHQLNAFTGRQFHRQ QLLYLRQTFVVDIDHHHPRLY AAVNGVIDSANAHRTCTRQQC NIAARFDAHAMLINILRGVIIGM ISTNNAAHRLCQRRRSKIRSRT GNTQPKLMQI

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29424	59792	A	29605	242	945	NGCIVRGKTSGSTFCVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL PSLLLALVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLGMGAQPPTPEWGTMLSDVL QFAQSAWWVTFPGLAILLTV LAFNLMGDGLRDAEDPKLKKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	1	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	A	29610	3	823	
29430	59798	A	29611	183	1163	
29431	59799	A	29612	4375	5125	
29432	59800	A	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	A	29615	886	949	
29435	59803	A	29616	123	315	
29436	59804	A	29617	34	343	HLCSYGRVYAADPYHHALAPA PTYGVGAMNAFAPLTDKTRS HADDVGLVLSSLQASIYRGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRGAHLRGRGRTVYNTFR AAAPPPPIPAYGGVVYQDGFYQ ADIVGVMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCHECFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1	273	FFSRVVPPIPSYQAQA/MVDIVT ALGWNYVLTASEGNYGESGV EFTQISREIGYPSLFGIQGCLHE CFAILCQVVYQFLLLMQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	



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29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCQVVSI MFSFNMFDHPIPRVFQNRFTQ YRCFSVSM LAWPNDRSDVEKG GKIIMPPSALDQLSRLNITYPML FKLTNKNSDRMTHCGVLEFVA DEGICYLPHWMMQNLL\EEG GLVQVESVNLQVATYFQELSSC YLPHWLMQNLL\EEGGLVQ VESVQPFKWATY\SNFQPQSPD FLDITNPKAVLENALRNFACT TGDVIAINYNEKIYELR\VMETK PAKPVSIHECDMNVDFA\PLG YKEPERQVQHEESTEGEADHS GYAGELGFRAFSGSGNRLDGK KKGVEPSPSPIKPGDIKRGIPNY EFKLGKITFIRNSRPLVKKVEED EAGGRFVAFSGEGQSLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHFFFQVSLLVFAWCSEM HG NRQLWERTGEMGRRT PGL SWTAKSPIGR/SLRSARVPRTV AHSQRAKGSHSLWVLRPQKRR CAGKSPPPSRLARSPRCPEPLVA LARQPLCVRRAGPEERARAQR RPPRVPLL SQPGRALLLLLLRS SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	A	29601	758	1076	LPMNRPPRWTGTILAPIIELLE LQQKENMALGSRTHHGSSPNS GSAFCQMACCSSLKPAL*SGRC SQP*WLWMSPLSRIFSISNSTSA SSSIGNAIRRRRSRPGP
29421	59789	A	29602	632	835	
29422	59790	A	29603	428	1214	FIAITVLPHWRSPQWYYPYWRG PVTALVRKVPAVAGERSLWS VVGLIWKPGLGLALQGVGFAVI GTFVSLYFASKGWAMAGFTLT AFGGAFVVMRVMFGWMPDRF GGVKVAIVSLLVETVGLLLLW QAPGAWVALAGAALTGAGCSL IFPALGVEVVKRVP SQVRGTAL GGYAAFQDIALGVSGPLAGML ATTFGYSSVFLAGAISA VLGIIV TILSFRRGQETAHQPDQQAAY DLQRSNRRVLPASPASACRCSD AHSR
29423	59791	A	29604	1	825	

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29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRQP GTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNVNPQQT PSHHPNLEHCPPFPKGEAGAGA WLRLRGLGSYEGLPGCALCFFF PSRVLGLRRCEQQEIAGQQQGR DTQHGQQ/RSAEGRGRPG*GPG RTGPPAAQLPQSLRTTTRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQQVKAK RSQQFDDECGEDVRQEHSRRD RVAVKS
29409	59777	A	29590	2	394	
29410	59778	A	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EED EAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEEANPFSTIRILF QLEQPALGTSQYKILCLST
29413	59781	A	29594	2	704	WRGGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSFNMFDHP IPRVFQNRFTQYRCFSVSM LA GPND\RIMPPSALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLENALRN FACLTGTDVIAINYNEKIYELRV METKPKDAVSIIECDMN
29414	59782	A	29595	1	1680	
29415	59783	A	29596	1	2220	

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29399	59767	A	29576	142	442	PKG VGRALAAFPQDRAPGPAA RHA*ASHPLHELLCGQSLPKR HPLLQGAQSHRPPKG*GVQAQ GTGTGRQLHLQPWCGIHWVKP AGLLSSLGPRCFYKL
29400	59768	B	29577	1	2464	
29401	59769	A	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL SPWVVDGTGCRGAGGGGAHRG GSGRTGAHGVGGR/PQAWQAA GPEPCPMGRQVRPGEKSSAVPV GQPGWGTQYTLRSHWLG
29402	59770	B	29579	1	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK PQPQPEERSSCAQGVGPPGGQQ ESQDEERSSDAPEDGPPGGQQK PQPEERSSDAPEHDPPGGQQQP QPEERSSDAPEHDPPGGQQQPQ SEERSNDAPGDGPPGGQQQP*P EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTRLRHCSR ARAQVKRMQRQRREREAKVR QPGTASGTSGIAERDSGKCSRK RGVQKVPG**NTRQSKLRPREQ CTTADP
29407	59775	A	29588	188	592	AAPRSPSYRMIRKTR*MLGR/E AEPHVCQQEHQVEALQHGGGP GETDATAAERR/RGRQRRQPGT ASGTSGIAERDSGKCSRKRGVQ KVPG**NTRQSKLRPREQCTTA DP*TLSTFPEGRGTELEPGFDSG ASVLMRGCRAALSASSPQGP GPQEM*ATRNWGRRQ*GRHC KLPVLITGLQGDVVEGVHVC ASQEPLIQNDQEDVDWQKA EPHVCQQEHQVEALQHGGGPG ETDATAAERRAGGKDASLVQH LVPAVLLSVTQGSVPEKEEFKK SLVNEILGKVNYDQGNVPPQ TLEHCPPFPKGEARSWSLASTP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29391	59759	A	29568	195	1899	GSASGVVRRSSRWARGLAGFRS EAADLHSECYSS*KQCGPKD*A EARFIAKSEGTKLPQCGRGPH*I QRFSTSPDSCGAQLASPSGSRTR AAGGAACQSWCRAP/STPQPLG GRWDWAPWSRGWRSSGTSGR TGAHGAGGR/PQAWRAAGPQP CPAGRQLRPETLKQNIILSLIQCI GASLVPTGTAELEPSPSLQLRGT TDAAQAIKNEFARVQKRNLCR RGPICFEGDALSWFFEKINKIDR RLARRIKKKREKNQIEAIKNDK GDITDPTEIQTIREYYKHLA NKLENLEEMDKFLDPYTLPRIS QEEVESLNRPTGSEIEAIINSLP TKKSPAPDGFTAIFYQRYKEKL IVLEVLARAIRQEKEIKGIQLGK EELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSQYKINVQK SQAFLYSNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLNEVKEDTNKWKNPC SWIGRINIVKMAILPKIEKQTNW NSQTLQCQPFCESDVCTSTLQIQ ERFEVAPLHKKALSSEEITDKT DPSPAIEELTV
29392	59760	A	29569	77	640	
29393	59761	A	29570	384	746	APWSRGWCSSGRLGLHRSPWS GWEAQAWRAAGPEPRPAGRQL GAMSKVETGT*DSEQRHFRG ESWGHWPWAGAQPTGPVLSGIL NVLSSFSVLALPRPTGWPRPCS AASPSRCPAQSHQH
29394	59762	A	29571	189	545	GLSCLPAGQGSGPAARHV*ASH PLHGLPCGSLPNEHHPLLHGA QSHRPPKG*GMAHDAAGLAGS STCSPGAGSTR*SQLGS*VCCTG RLVGTTQLRPESG*VSQSPRL WAAAEAGSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I CEGRTCFEEPCNCSSLYVRSNG GNHSHSTTTFKYNGSNWIPRW QGPGSTQPSKARRPVAFSQGN CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	B	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS LGLSCLPVEQSGSPAARHA*AS HPLHGLLCGRSLPDEHRPLLHG AQSHRPPKG*GMRAHGAGLAG SSTCSPGAGSTRNREN

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29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH LVLCLRHTAGVQ*SWDS*SGLT PELV/HLDGSHV/LAASPRGSPG/ SPK*MGADQRSESSPGPQGG PRAEGPHHIQEAPRSA*AQGAG AEAARLGAGQASGCQSTRRPA GSRREPGVSLDGGHRAVVGIQF QAPSRRAAWGHPLHDAPGRRL MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRKVYVWPQCRPTG AVLDFSPGCSCLEPAGQGS GPAA RHA*ASHPLHGLLCGPLPDEH HPLLHGAQSQRPPKG*GMRAH SAGLAGSSTCSPGAGSTR*SQL GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ KLLHFLYSLQKGISPNAIPPHSP HPTTAPVYSSQCERRRRQVISAF PT/GD*SLHSN*E*QGGVEGEAP AGTWAVRGA*GPAGVPGGRGL GGLRTRSSWPALLAPGRQGS GP AARH/GLSLPQPPWAPVQPEPP* GAPPPAPRRPVPSATQGLRSAS ARRRTGRQLHLQPPCGIHLVKP AGLLSLVGTWRVFMS
29389	59757	A	29566	1	470	MGQPLLLVRDSSGGLQLWQKV KGEPVQQHERRIIPPAREEKVK RSPAGPPPSGGLDSSRHKIPSHE QA/SGVQPACRTNHQPRGIWCS PSLPDEKCPLLHSAQSHRSPKG* GVRAHGVGLAGSSTCSPSAGSN G*SQLGS*V*NKGR*IYPTGRC
29390	59758	A	29567	777	1063	QLPPPSVFPTTPKTELVLGTPGH GQPHRGGHESSDSAGGHLP/LR ALRSGWDPSPSSVCATPTSSGL SSTPQLPLHQR TSSSTASWSPG WGMGSC

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29368	59736	A	29544	175	355	FSQQLLGQAD**SFL\GCSRLL TAVSRPKRPGEAGITPRVRCLLS NMKDILVASKFWQL
29369	59737	A	29545	482	1196	
29370	59738	A	29546	196	818	
29371	59739	A	29547	170	370	
29372	59740	B	29548	147	257	
29373	59741	A	29549	1	1278	
29374	59742	A	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCDVH*LSL DVLPRGCA*HRELCIHDLLKGN PLRRNILAG*TQERMQLQVESQ SIPEEILGLQPQLGPMGGLWNV RFLLIPTVLWGFHCSQERAFPR KLQVKSFPVAQG
29378	59746	A	29555	149	381	
29379	59747	A	29556	1	656	
29380	59748	B	29557	146	1320	
29381	59749	A	29558	629	1417	WCASHWGS GHAARHA*ASHPL HGLLCSPSLPEEHPLLHGAQS HRPPKG*GM*AHGTGLAGSSTC SPAQGL*IHQSAPCV*LKVCECT NRHSVSSCDEDVCICSLCLGQ* GP/ECI*CRIFLGPFNRLIEGAPH L/CRSAMLNPLQEGAREQASAR SGWLLRLLTQEQLLCRACIQTR RDREGKTRHRKGTPEIGKGRAF WKKSLKIILIFNCLRYWNA YM EIWVPALTGIPPNTVNYATSSS KDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APP PASGHPVPSTTQRLRSAGARRG TGGQLHLQPRCGDPLGETSWA PESRRSAASLLKPARPRAHWEE QTTPDALL
29383	59751	A	29560	88	564	SCLPVLRRALAFSPWVVDGTG RRGAAGGGRWGGSRTGAHG VGGRLRHGGLQVPSPALQEGS* GSVRNRAQPGGLALLGDPVHP LQPLARVLSPSLP/DQQGWPA APSVGPTKPTPTRNSSWPPSAA HSPGSCSCLSLHTSLESCRCPSIN TSLHKHA
29384	59752	A	29561	3	339	RYKDSRPHQTQEPSWLHLVDP APRLQVELPASPALCARIPQLG GHGTGRRGQGAALVGEARAG LPSLPSFFFSLLSFLSFFLPSFPL FFSLFFPCPVNCGEQCPIGKM

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29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTQPDNPFSDPKLKRMSKS VPAFLQDESDDRETDTASESSY QLSRHKKSPSSLTNLSSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKELVHVFAGP VEGLNSSGWKKTGVIPIY*KGIV LLPNKGQMGKKTLVVKKTLN PVYNEILRYKIEKQIL*TQKLN SIWHRDTFKRNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRK AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	B	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	A	29529	1	2769	
29355	59723	A	29530	450	3061	
29356	59724	A	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSERRHVFGESEDELIGQ KVAHALAEGFRE*FACIG\EKL DER\EAGIH*GRLFFEQTQVIAD NVKD\WSKVVL\AYEPPLAIGT CKTSTPQQAQEVHEKL\RGWLK SNVSDAVAQSTRIIYGG\SVTGA TCKELASQ\DVDGFLVGGASL KPEFV\DIINAKQ
29358	59726	A	29533	1	929	
29359	59727	A	29534	3	623	
29360	59728	A	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCFLCILQVGRAHA FLLCSDFMPCFAVCSSIIYSFIPV TKTQGAAPHTRAHSLTPDPKPS CCCCCPRPGEDPGHMCVWWP WQPSVIYAKYWTYEHAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSGRESQA
29366	59734	A	29541	1364	1916	
29367	59735	A	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFS\RYSGS\EGSTSDP *PKGEVLKVLMDKELPRLSLQS GKDKDAVDKL\LKDPGRPMGD AQGGTFSEVHPCSVAAITSA/C HKYF\EKAGLKLMPWEMFTDF LGQSIGSQGFPMFCLGIYFP

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29336	59704	A	29511	1	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVP EECKMF ACAKLAMRPPSLIRAGSRVAY RPIS\ASVVISTQRLSRTG\EGST GI*MGPQNGVS\QLIPKGSFQTS CNQAGGHLITGCQIYL GAGCLQ Q*GVGWFLVAGIGNSLLGKPYP LGYGQKTLSPESQQLVPP*CYP GDFALALKLKAMGL\FCLMVA FLILFADVTEITA
29338	59706	A	29513	427	840	
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ*DGTL L\RR CGS*GLPTFKKSTCGKCGYPAK RKRKYNWSAKAKRR\NTFGTG RMRHLKIVYRRFRHGFREGTTP KPKRAAVAASSSS
29341	59709	A	29516	1	668	
29342	59710	A	29517	649	992	
29343	59711	A	29518	1	2994	
29344	59712	A	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPRSRRSKRDLIEFS CRIILFPLPSLPPRISFHPSPTLAR VRIGGA VRRPHQSHSISSSSFGA EPSAPGGGG\SPGSLPRPWGPKS CSSSLCGARS*FFWRDVKN TGL VFG\TTLIMLLSLGSFSVSSVVV S\YLILGFSSSVHHQLSGI*QSSVI PSCNRKFRKKGHPPFQKPNWNV DITLSSKSFSINNMNAAMVHIN RALKLIIRLFLVEDLVDSLKLAV FMWLMTYVGA VFNGITLLILAE LLIFSVPIVYEKYKTQIDHYVGI ARDQTKSIVEKIQA KLPGIACK KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS VAWNLVFCIRFLENTVGIVTI*R RCPIPFSAF
29348	59716	A	29523	1	4368	MLFSYLEKYFYVADEL SHC VEP EPSQVPGGSSRDRQQGKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDFNRSSYSDDNK/LI PPTSPRNRVQRKNR\PKSQVAV DLVTDDTTLRENGSKTLSPSKIE LKPVRSDSPFQAEGDMLVSESC QDNNVNIKSKFMNLSQKGTPK EGPGILQPFESYGTPSQGSKNM DYSQDSKSPGKNGASPSNSNY SYSVLKESDAENQVPCNTNIG NLGEEEPKFHAH



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29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCTPTPYFHDPTPFPLFW KELATCAGNLATGTRNAGSPG FLLSRVPSVWDPTENRTVQLT WQPLPELELWPKA/HLTDSFP DLLGLAA\ED*HCTIASEAP*TI\ TDAELWVTL\TVEGKPFPLINT EATHSTLPFFQ\GPVSLASITVV GIDG\QA\SKPLKTPQLWCQH* TIRRFKHSFLVIP\TCQVPLEG\IE DTLTKLSASLTIPGLQLYLIAAL LPNPKPPLRPPLVSPDLNPQV*D IGVEWGKGD
29327	59695	A	29502	6958	7935	
29328	59696	A	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFYKGCSCFH RIIPGFMCGGDFTRHNGTGGK TSKKITIADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKVPKPAENFR/A L*SIEEKGFGL*GVPCFHR\IIPGF YVSRGGDFTPP*MAPGGQVHL MGKKFER*RTSSLKHTG\PGHL VPWANAWTQTQMGSQFFICTA \KTEWLDGK\HVVV\AKVKER HEILWEAMERFWVPGNGKTS KKIISIADCGQLLISFDLCFYLNH QDHSLLCSPLRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCCSPCRRRLGREEAGEEPTSP VTQYLQPRSPREECKMFACAKL ACTPSLIRAGSRVAYRPISASVL SRPEASRTG/EGAATVGVAGSG AGIGTVFGSLIIGYARNPSLKQQ LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSPREECKML ACAKLACTPSLIRAGSRVAYTP TSASVLSRPEASRTGEGSTAFN GAQNGALHLMQRELHTSAIRRD IDTWCKFIGCSAATE
29334	59702	A	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNRJIICFHP ASLVSLY*QPQLASWTMCKQD ENTQEGKSWDSFSRDVIHI

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29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLTPN YPDRQPWTDKHPDLLTCGRCL QTFPLEAITAFMDHKKLGCQLF RGPSRQGQSEREELKALSCLRC GKQFTVAWKLLRHAQWDHGL SIYQTEQRPRRPSWA WPRWL QPCRQWWGQQLRPAPV/HSG SGLTRRSPTCPVCKKTLSSFSNL KVHMRSH TGERPYACDQCPYA CAQSSKLN RHKKTHRQVPPQSP LMADTSQEQA SAAPPEPAVHA
29316	59684	A	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	A	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	A	29495	39	1092	
29321	59689	A	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/ TLRPKAL*LTSPQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
29322	59690	A	29497	1	281	VSDHAGTPALVLHP*RQVPLF* GRGKYPSTPSPSPLAELATSAR NLTTRPRNACSPGFLPSRVPSVR DPTGNRTVQLTWQPLPEPLEL WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCPRSGALRS GDL PWEINPLSSCSLLHEKDPP MTSGPQTNQPKHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPTS SY LCAPIPYVRTPTS YLCALTPFPL FWRHIRT SKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGM PAAQ
29324	59692	A	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD AEL*VTLTVEGKSV PFLINTEAT HSTLPSFQGPVSLASITVVGIDG QASKPLKNE

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29308	59676	A	29483	13	945	NRGPAGVPAAAAMQKYKLE KIGEGTYGTVFKAKNRETHeIV ALKRVRLDDDDDEGVPISSALREI CLLKELKHKNIVRLHDVLHSDK KLTLVFEFCDDQLKKYFDSCNG DLDPETVKSFLFQLLKGLGVFCH SRNVLHRDLEAPATWLINREW GSWKLGDGPGVRAFWGFPV RCYSAEV/VSHLWYRSPDVLF GAKLYSTSIDMWSAGCIFAELA NAGRPLFPNGDVDDQLKRIFRL LGTPTTEQRPSMTKLDPYKPYP MYPATTSLVNVVPKLNATGRD LLQNLLKCNPVQRISAEELQH PYFSDFCPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKTIADCGQLE
29310	59678	A	29485	3	1225	
29311	59679	A	29486	1	864	
29312	59680	A	29487	1	1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSIHGEKFDDENFIL KHTGPGTLSMAIAGPNTKGSQ FIYTAKSEWLDGKHVVFGKLSR GDSLKEPTSIAESSRHPSYRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTSTSYKSLANQTRNGSL YDSLLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAER HPRLVPTGPTHREPSVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPLGKTPLGRPAV PRFGKPDGLRGRGVGSPEPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLLTpkDEVQLKTTYS KSNGQPKSLGSASPGPGQPPLSS PTRGGVKKVSGVGGTTYEISV
29313	59681	A	29488	1	3126	
29314	59682	B	29489	46	114	

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29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPEFLPS GGFVVSLTSGVKLQTFTVNVTA HKGSVDPKRVKLKTLAVSVTA LKAACLELFLPPGGFVVFAGFR SEAADLCAEGASSGLGQPREGL PRCSGGLKGSSAARMGAEAK GAPRASQGCEGRHHA VTSHRS DMGEEEGESQRYLSCPQPSCPI NLLQEDASKVIVFAESGINPDSV LDLIMLH
29297	59665	A	29472	335	453	KYIWNVNLQHSVSMML*FITS*L SGMDSLFPAAHCV
29298	59666	A	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDAVRFYP WTIDNKYY SADINLCVVPNKFL VTAEIAESVQAFVVYFDSTQKS GLDSVSSWLPLAKAWLPEVMI LVCDRVSEDGINRQKAQEWCI KHGFELVELSPEELPEEDDDFPE STGVKRIVQALNANVWSNVVM KNDRNQGFSLLSLTGTNHSIG SADPCHPEQPHLPAADSTESLS DHRGGASNTTDAQVDSIVDPM LDLDIQELASLTGGGDVENFE RLFASKLKEMRDKAATLPHEQR KVHAEKVAKAFWMAIGGDRD EIEGLSSDEEH
29300	59668	A	29475	1	1773	
29301	59669	A	29476	1	1023	
29302	59670	A	29477	2	616	
29303	59671	A	29478	1	972	
29304	59672	A	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG EGTYGTVFKAKNRETHEIVALK RVRLDDDDDEGVPSALREICLL KELKHKNIVRCAGGGCSLPVW PLGGGGG*HWTSVRRTCLAEPF FCPRLHDVLHSDKKLTLVFEFC DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	A	29482	1	873	

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29278	59646	A	29453	1	599	
29279	59647	A	29454	1	504	MWNCLTNKLLFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHSG\NIT FDEIVNVAQHMWHRSLARELS GIIKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSSGR*KTTSFPAKLFN ACRISLLASAEVNPINISAYLAT WISQIPSCSCRVPSDFLIWSTNR YSIRF
29282	59650	A	29457	1	801	
29283	59651	A	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTFRKSV YLEVAPKGE\VGA\TSALGPQRI GP\LGPVSKKKLG\DDISKA\TG\ DWKGP*GITVKLT\IQNRQAQD *GGCLSASALI\KAL\EP\PRDR KKQKNIKHSGNITFDEIVNIAR QM\HRSL\ARETLWNHLKRSL GTAQSVGCNVDGRHPHDIIDDI NSGAVECPA\SDIFIVTVGVKG GPPSVFTEISWEVLEMTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286	59654	C	29461	181	381	
29287	59655	A	29462	427	957	
29288	59656	A	29463	3	241	WLRAERAPEGSPETKGS\PPPPP RSVLHLSA\SSPGLRPPEGL*TC RGSPSADSPRRGKHGGKTTHLV SWLSQQKIPMAR
29289	59657	A	29464	122	473	
29290	59658	A	29465	1	771	
29291	59659	B	29466	1	1017	
29292	59660	B	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQQRYECDNQQPLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	A	29470	321	2645	

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29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCCLVFCPCDTLLRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYPSLNF
29254	59622	A	29429	667	834	
29255	59623	A	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLPHLVFGSHSGSLWEL LSH*VYLLILSLPPHTPQQAPV WDVPLPVSCKSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVTGTGQGCHRG PAESDGPAGGARHWEQPPA*Y LVFLCSQRRWPGRQQRGQSG RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AIGTPSRKPSP STAHVKHRRLCIPTRRGFSSDN WDPVSSPTCNDARQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFQGS*LLCI GLAHAPLAQRSLLLSTF*CLLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGFRNFQPFCSGFSS
29260	59628	A	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIIEGSLVLFHWSISLFWYQ YHAVLVTVV*YSLKSGSVMPP ALFFWLRIIDSAMRALFWFHMN FKVVFSNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSYTRKIQLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSLTGVRSIIT
29266	59634	A	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	A	29443	531	845	
29269	59637	A	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGGRRSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCPKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCCCC RRCPSLGSDAGTELETQRPAG TGPGPTVAPATFLQSRRLMVGA GTPTLGVRTPGFGLQLGFFYWL EDVERDTS
29275	59643	A	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

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29232	59600	A	29407	1	1483	MFVLADFGHTRRTNRS LGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPMTRRVKRHNTVPLS FADGYPYLLANEASLRDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVIRIGDVVFDVVKP CSRCIFTTVSPEKGQKHPAGEPL KTLQSFRTAQDNGGGEGEARA ANTGATHRGRHRSPSAVRYRD RLNMYVLRRMDLLYRVKTLW AALRGNYHTWPAIDITLPGNRH FHLIGSIHMGSHDMAPLPTRLL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQQLQNLQ HISQEMGISPSLFSTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHKPVIELEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQQMRAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*RKPKNTENRRCISASVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIAWTN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	
29235	59603	A	29410	441	583	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIIRAPRRLHSFLLLLLLLLLL LLLLLLLLLLLLFHLSSSSFSST SSSSSCSRFSM
29237	59605	A	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29240	59608	A	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	A	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	A	29422	409	543	
29248	59616	A	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

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29221	59589	A	29396	1	318	MEKKSPAYFCCRDMQVIHSDA ALQRLLTRFNDPEGWSNLAKN QYLSTSMKQKIWQRALSHRKN NPKADSDAYETSADMILSELIS HGEVDDQMLLNATALIRSDDW DFLESALISWDNLPVVLKELQ QNTPRNDIWAKFFLRQENSSRA QVDEALRVYYALDPDALAQLD VLAKRPYKTAAFRGEKTHRVP RRSVRQNIIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHHQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYKTV RGLTRGLMLLNMLNKL DSTSP CRMLVCCVPRAPPNPGGLNPR AHS LN RSP*NPLKLLSPTGPFEG MRPLGTHFWGGIGHGQGPEWG PQFGLGMNLLVKSLGHWATW VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMHGD LGISMK SRIPVWEEFVPRFQATLELGVC AMIFATAVGIPVGVLA AVKRG S IFDHTAVGLALTGYSMPIFWW GMMLIMLVSVHWNLT PVSGRV SDMVFLDDSNPVTGFMLIDTAI WGE/DHGTFMGAAPIRILPAYG LG TIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVIVHA LRNAMLPPVTVIGLQVGTLLA GAILTETIFSWPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	A	29398	187	1710	
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTFIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	A	29401	406	1023	
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLLEKMRES GDIHSHHGWLHLPDHKAGFSE EQQAIWQKAEPLFGDEPWVVR DSPGYFALMVRAKFNNCVIVFR R*AQQRHRYTDVVVEIACRIKR VAALA
29229	59597	A	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	



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29204	59572	B	29379	54	275	
29205	59573	A	29380	2	215	IFLLLLPPHLLLLLLLLLLLLLLLLLLLLLLLLL LLLLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	A	29381	100	393	FLLLLLLLLLLLLLLLLLLLLLPLLL LFSSSFLLSSSFFFLSSFSFSF SFSSSPSPSPSPSFLLSSSFFGV ISLDVVTLAWQSARITGVSHRT
29207	59575	A	29382	264	911	ILGFLRDGNFWRKSQSFFPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VG DYRCEPPLTKRNIFCILSEA TDITY*LTSISFPGFCFRLT*LLPL TEITGEAVVQIPIKFCPMCFQ CAKIWTRGMQWHLEAWRCQK PQSPKGGVTALAEAPKSGLLE GQFMPMPQYLAVQKKVWWF DVSVDSEKLVNRVYG
29208	59576	A	29383	1	261	
29209	59577	A	29384	3	195	
29210	59578	A	29385	1	399	LERLSAPCISLLLSRSLSSLSLSS LLFFFFFLLLLLLLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLLLLLLLL LLLLLLLLLLLLLLDPPGDTIQGA PSRGYHPRDTIQGAPSRGHHPG DTIQGVPSRGYHPGGTIQGAP
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLLLLL LLLLLLLLLLLLLLLLLLLLLLLLLL LLLLLLSSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFFF/C LLLLLLPLLLLLHRKHLICVTLG CLRWLQQLCVRLQGSCAWLQT LGWVHTYACVCTFFLDQQVAG RILLVEDPRSSLLQCCLLLDA/P LCCRFQKNMHFIRT*R*VHCSGI TSIQFNLEP
29213	59581	A	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLLLLLLL LLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	A	29389	3	264	
29215	59583	A	29390	296	421	
29216	59584	A	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAATLFFLFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLFLF L/VPLLLLLLLLLLLLLSSSSCSP PPSSSLEKLYLSI
29220	59588	A	29395	3	2368	

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29193	59561	A	29368	1	1815	STLEDPHYHYHIAEVSPVVIISY GATGEKYGFITYRCSEHAALSL TKGAALRKRNPSFQLSYGGLR HFCWPRYTDYGYFELQINRLAL FSTNVTAEPTPYMHLAPPVGTQL PLPHLSHDNSSKNSGGCLPGAS VSCNYREPAVRLALASTLPLLR AQSPFFMHKDKDPLFWFLTVP KWFRKGEVILSSRPRKKTEGSW FPKTFGFGKSHVLVKEFYNRK HHIAKQQHAVERTRELFCPKG LGYSKPQTQGDYIAIAQH/L*T NLPTGCWAKYAVISFMRD/TV DDKHWP EEHLAKN*LGLLADS GIRIKLPWGAPHEEERAKRLA EGFAYVEVLPKMSLEGVARVL AGAKFVVSVD TGLSHLTAALD RPNITVYGPTDPGLIGGAPENG DSDSALYRLKEME EFHLVVG SDIFGKHQHGTTETDSTTCPSTLE EFETQWFITGGINRILLATDGDF NVGIDDPKSIESMVKKQRESGV TLSTFGVGN SNYNEAMMVRIA DVGNGNYSYIDTLSEAQKVLNS EMRQMLITVAKDVKAQIEFNP AWVTEYRQIGYEKRQLRVEHF NNDNVDAGDIGAGKHITLLFEL TLNGQKASIDKLRYAPG
29194	59562	A	29369	3	1993	
29195	59563	A	29370	1	1782	
29196	59564	A	29371	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWMGYQMLRG ALKKEAVSAPAPQVELPKSGRS FLEAIHYFGSVFSLFVGDNVGT ARWGIFALIIVETLAWFTVVAS LFALPQMRRGYQRLAKWIDGF AGALFAGFGIHLIISR
29199	59567	A	29374	50	620	
29200	59568	A	29375	194	767	LWW/AGGLYLCWMGYQMLRG ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLANPKAIHYFGSVF LFVGDNVGTARWGIFALIIVE TLAWFTVVASLFALPQMRRGY QRLAKWIDGFAGALFAGFGIHL IISRLALIVPGLLQKNGGWRM AIISAVIALVCHAILEARILPDG DSGQNLSLLNVGSLVS
29201	59569	A	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	A	29378	485	1166	

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29188	59556	A	29363	1	986	MKVTFEQLKAAFNRVLISRGV DSETADACAEMFARTTESGVY SHGVNRFPRFIQQLENGDIIPDA QPKRITSLGAIEQWDAQRSIGN LTAKKMMDRALIELAADHGIGL VALRNANHWMRGGSNWQQA AEKGYIGICWTNSIAVMPPWVP KECRIGTNPLIVAIRSTPITMVD MSMIKHTLPQRAAGTDRKLAM SREAQLLERHGYAFNELDLGK REPVTEEEKLFVAVCRGEREPV TEAERVWSKYMTRIKRPKRFH TSLGGKPPQGGKIVIRPLPGLPV IRDLVVDMGQFYAQYEKIKP/V PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THQPARRFPAYHYAHPAAAAA PGDPLGADLQLCARHYHRQRH CVPRHAGYPRSDGLHPQPRGR WRJRCSDCLRV\SDRGDAGDY FHL*LADR
29190	59558	A	29365	871	1206	
29191	59559	A	29366	1784	1966	RPLDVFSMSSFTSNSPLTDLVG YLTFSAILSWRLSLLSDAA*TP YPPWGSVHCRRFCSL
29192	59560	A	29367	1	1276	FHIKLVLTGATWTALPYCHSHV GLRASLKPTPPFWGRAPLGRTP SQKTECRLINFPETPIFGNSFK YDIEVSNKSPDEEVKLRHHLA RCMKNFKTDIYFVSTFEPSTKS VDLLTVETFAGTVCEYADMPK EWTTTRGLYDPTHLISASCHKV EGLFSFEDRTVATLIRLFIHPVK SMRGIGLTHALADVSGLAFDRI FMITEPDGADIAVKTFTGIRLKV PCPPDHPAFSITNHQTEVTALV VFECDIAVRGSDRLRLSPGGG SNTDWWIFGLLIKENPGSLLAV GVNLLGKILLSVVAAVSESGQN FLSVLPVRSEGPCFVVIDVDVEL PGLRDIADDEVKTGVIAVTPAIVP ALWEAEVDVNIAAFRSQKAYIS GQVNKSGQQAITN/DATDYSRG HQKLPLCLQSECFHGIYHRIDVA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29172	59540	A	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELRDRRLNFEWWK PEYGINLYQDYKQDGFVEIPD QNNPSLGDMMVIMQIQNVVPVW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNVG HHEEEKFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAAFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPPQGWRFV QSSKNKPSYAFGGAVNTTGGGI PSPGPVWISRRRWRNFLSRFLC RGYELKLTRLARVFFRLYNES
29175	59543	A	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP\PE DTDLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPPIEIVLKITI
29178	59546	A	29353	1	2346	
29179	59547	B	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	A	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHDRHHWH\GNRE NKVNCQLICVDIIINTAQPITSES /DQRQH/TLLRRQTRDRRHWS HEP
29185	59553	A	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLP AQGDSADPHPGHSFLHADNPA LPDPVGVYPEPQGA VRLLDIGQ HHHPWEHGS DL*VYHGGDSIS QQPTLDGKLEDLLAVLWYSHL
29186	59554	A	29361	467	3014	
29187	59555	A	29362	1	1174	

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29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLLWKLEAAGSP LRPLSVQVTTTPQEAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQIR GAMLDELAAVTGCRAACDAT RVKWHRQ*GNWSRNLAAPR KLR*RVN
29151	59519	A	29326	1	2349	
29152	59520	B	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	B	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	A	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	B	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNTT**A SAPGN/ARWNSYVG*KHH\SCQ WGDYRRQCFRGE
29162	59530	A	29337	1	3189	
29163	59531	A	29338	1	1344	
29164	59532	B	29339	1	1233	
29165	59533	A	29340	1	1572	
29166	59534	A	29341	1	3591	
29167	59535	A	29342	1	843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRRREIRDAATLL RLGLAYGPGGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTAISAP/GGGS AEWRLHMGYDPHTFTDFELTDSR DAERLDRFAQTAD EIRIADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGMRFDMMGFL RGLDCEVPDPKRRNTSLWRITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRILQMVQ PLS
29168	59536	A	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRISKAHVISCVAGHTLA AAPQPHYFTRETYSPEVSTLM TSPICTNSGTLTTAPVDRVAGLP PVPAVSPFRPGSVSTISSSTKFG

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29140	59508	A	29315	1	2237	MLTGYRAVSRHKSQRYTADDA EEMIGKLTGMPIPLNSLRQWIL GLPGDATDYKLDDQYRLSEITY SQNGKNWKVVYGGYDTKTQP AMPANMELTDGGQRIKLKMD NWIRADGYHTLQTLFQFLDYG DTISIELRDDGDIRLLTPVEGVE HEDNLIVRAARLLMKTAADSG/ LSSDGKR/RSSSCARVQSPVSFF GNWWMLGQTTTRVSPLCHWAIS SAISHRRAFAQVINIRFKRQTKA GDFQFTGAFIGSRQAISHRRFHL IDNPERFVIVHFARGTDKPRLLG VLCHDKPRINSNAVTAHARAR LKNINARVTIRQANQFPDVNPLI GTNQRHFISKSDIHIAEAVFEPSI IAADRLNPLVNELIIMPDIKRL DAFVRIAHEELLYLLGILMNPA NKDHVLPILITGPKESADYFRV LDEFVVHTLGENARRHYRIIDD AAEVARQMKKSMPLVKENRR DTGDAYSFNWSMRIAPDLQMP FEPHENMANLKLYPDQPVEVL AADLRRAFSGIVAGNVKEVGIR AIEEFGPYKINGDKEIMRRMDD LLQGFVAQHPSYNDLLLMEI LPHLLVEGMLISAVSAESLPWL HLSCVANISKRQLICAVPLPKPP KAGLLGKNIMGTGDFDFELFVHT GAGRYICGEETALINSLEGRRA NPRSKPPFPATSGAWGKPTCVN NVETLCNVPAILANGVEWYQNI
29141	59509	A	29316	1	2892	
29142	59510	A	29317	19	649	
29143	59511	A	29318	2471	3036	KVTWVTC SILPMTLSPSAAFSSL FRMKILSLK**KRILR/SSGKPAA RQGDMTQYGGSI VQGSAGVRI GAPTGVACSVCPGGVTSGHPV NPLLGA KVLPGETDIALPGPLPF ILSRTYSSYRTKTPAPVGS LGPG WKMPADIRLQLRDNTLILSDNG GRSLYFEHLFPGEDGYSPQRT VACAPRRGKTG
29144	59512	A	29319	1	1476	
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVLSPL*PNFRT RPF RPSSVPR**PKKDLKIATSA MMEAA YSSVIANVVLVPVMDA KWLAR
29148	59516	A	29323	3	260	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29139	59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGNA DNANFGKAVPADFNNGSFGRGD SDEWTFGAQMEIWCSYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRGCAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQLPDATLC VLSGLQTEHNRRWPNSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLTLLSPESDLYHFERDD FWFPPGDINGREHHLHIILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAEDGSVMT LRSFLDKDGHPIECRGI*PIKAR HLVRLMPVLRRLRECPVLMRR IR\NGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNYAHL PTIFAAQRKIKDADLPSPQKLDI LQETIAFLTQSGYQFIGMDHFA RPDDELAVAQREGVLHRNFQG YTTQGD TDLLGMGVSAISMIGD CYAQNQKELKQYYQQVDEQG NALWRGIALTRDDCIRRDVIKS LICNFRLDYAPIKKQGD LHFAD YFAEDL KLLAPLAKDGLGDVD

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29135	59503	A	29310	1	776	MELAAALRSENQPDEKPLGETL KDLFSRPVLPMTDVLPLNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDIDSSQ GIVDASGTAHLSDNWPVDITLN STLIVEPLKGDKVKLKMGGAL REQLEIGVNLSPVDMDLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSMPKESGADEKNSDNR WCRVYWLGAALYHQRNERR GGSGR*ADLRRKPDVAGTGRA KRALCL*ES*YLRSGRTGTRIH
29136	59504	A	29311	955	1095	HRRHPIPFLIHHRDQPFHQRLK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRRPASGRYP CIPAFVGTPAVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWGLADRQANPAQVEIIEIRQ L/VRKSPQTAHSPARIWRRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSGKYQSRRRARRPASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQTL SLSDKCRQGTVSGRLSLRKSDC TPISHASCSSSLHGH*VSVAVR LRMTDFSRTVGKDVQRFDAGL GWTLELLSAHAAFRVALKAG DMAILASRPPTVTPNSMRLGR LYRSGVYGR



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29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN ASGHAKRQSDGDLRSRAATGG DHSAGDWCGRRVQTSAG*LWR KARPWPNR
29125	59493	A	29300	2353	2758	SQAYHQVLPVCEAAPDDNHT LAALR*HGVYEKHMDDQDCWA SFLPEERLFWRPAPRSDRVEC VDSLPLTAVGKVDKKQLRQWL ASRASARAQRRSPLAEARKPQY VHQGMDNARTALQKPEQARA HTEVHW
29126	59494	A	29301	5	793	FLQRFVADLPCGAQVVKFSTFR TQCRQTEATLKVLFHGTFFNVV TSIGATTQVTNDARTDLRKQLV IDILFGIRRQTLHFLDRHNRHF CRCSRNTFLFQLLRMIRDFND FELVNPLSLDSVLGMQPLREEI QQADRDDDKHHQGAGLLELET ANRFPQGDADPACADHADDGR RADVGFEAIEGVGDQQWHHL WQHAVEDLFELVGTGGANAGP GSIASTASESSLESTPVVWINSA STPARQRTGRGRRRPRTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	A	29304	1	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC* WTLSPPLITN*L*STSITSTSAVA SASSSCARVQSPVSFFGNWWM LGSTTRVSPCHWAISSADF
29131	59499	A	29306	2	696	VPAGRYTGRDLHLHI/ILPFRES LPARHRVRRYRPLEAC*TPCTD GYHRIFYRLKGESAKDGSVMT LRSFLDKDGHPIEDINDQAR HLVRLMPVLRRLRDARFMRRIR NGTVPNVPNVEVTARQLDFLA RELSSHQNLSDGQIRQGLSAM VQLLEHYFSEQAGQARYRLM RRRASNEQRSWRYLDIINRMID RPGGRSYRVILLGLFATLLQAK GTLRLDKDARPLLLIE
29132	59500	A	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F AVVSGSEHAESDAG*SGELLEQ LSEVLR*PDEIFLWRCRAEREQL GL
29134	59502	A	29309	236	645	

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29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLSNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSSSTSS SIIIIINSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	A	29275	1409	1641	PENGRPVYAGGRDAAWRDVY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSA LGLCL* RLAGGDWCRDYSL
29101	59469	A	29276	1	3252	
29102	59470	C	29277	1	2760	
29103	59471	A	29278	1	723	
29104	59472	A	29279	14	338	
29105	59473	B	29280	1	1201	
29106	59474	B	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	B	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDLSLRHFKDTSTLY LEIVDYPGEWLLDPLMLAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLHHCKEQGLHFI QPGRFVLPQDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMR WPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	B	29286	1	813	
29112	59480	A	29287	1	546	
29113	59481	B	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117	59485	A	29292	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFFQHL*VPSGTSP*L*H LSGILWHFLLQALLYPRVFLVL LCRSLGAVCLY
29119	59487	A	29294	1	2046	
29120	59488	A	29295	3	654	
29121	59489	A	29296	2	182	
29122	59490	A	29297	1	1215	
29123	59491	A	29298	141	266	

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29090	59458	A	29265	1	2416	MLAQSLQALEQDGFNLRIAYPV VPPHVEYSLTPLGEQVSEKVAA LADWIELNLPEVLAVRDERTRY DIAVPRKRYGHAVSRNTFALRS QERYGHSVLETVGNSGSSKQFS MDILDPCARGPGQISLITVNHKL HVRCEIAYSVQTMVVKGSSA FAAFFIAVVLWMIGYVPNVEQS TQALLGMQFIMIALPTLFFMVT LILYFRFYRLNGDTRLRIQIHL DKYRKVPPEPVHADIPVGARLS FAERVMEGLSDGGQSLQSPSAL FSKQTLKNMSIYKIPLPLNILEA ARERITWTLNLTLPVCVSFSGG KDSGLMLHLTAELARQMGGKI CVLFIDWEAQFSCITINYVQSLR ELYTDVIEEFYWDALPLTTQNS LSQYQPEWQCWEPDVEWVRQP PQDAITDPDFCFYQPGMTFEQ FVREFAEWFSQKRPAAMMIGIR ADESYNRFVAIASLNKQRFADD KPWTAAAPGGHSWYIPIYDW KVADIWTWYANHQSLCNPLYN LMYQAGVPLRHRMRICEPGPEQ RQGLWLYHVIEPDRWAAIGSP ADREEDAEYELEAIMEARVTV AGMGLVMEVQDYFDGEADRL AKAWLP EYTPQIKSLKDERKE AYRQIVEMSTEPQDVLVRPA NKFEMTRVREGEKEADLPVWK HHLLCDESGNYPALLNHWETK VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	B	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	A	29271	17	352	DLQDTGCFMLMNTGEKAV/KS ENGLLTTIAC/GPTGE/VNYALE GAVFMAGASI/QWLRDEMKLIN DAYDSE/YFATKVQNTNGVYV VPALPGWSLLWTRTCHRIFPRH RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIELN TDFLCLINHMVVGQHIAFTGVD DDTGA*TFEGLCLIR
29098	59466	A	29273	1	975	

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29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSPLPSSFR STRVR*EVSGRSSPSISLASLVR PIT/SLLIVNAHPVELLQVVFPTL DKHIAAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPT AVDLFFHFNAVTKGFHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	A	29251	1	177	
29077	59445	A	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	A	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	A	29259	1	927	
29085	59453	A	29260	1	1113	
29086	59454	A	29261	1	875	
29087	59455	A	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	A	29264	1	912	

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29066	59434	A	29241	1	1605	MKVPRGDVMFQLNLRKDDGQ FEDQLLLLVLPPKHRGHLQLV ADDVWFKNRRAKCRQQRQQQ KQQQQPPGGQAKARPAKRKAG TSPRPSTDFRSRDGIPEKATRTS CPSDSSVFSLQRPPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFEKRLEVNVNHYFTTDD GYRIISARFGVPRTQVRTWVAL YEKHGEKGLIPKPGVVSADPEL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVYEERGE AGLRALKIGTKRNIAISVDPEKA ASALELSKDRRIEDLERQVRFL ETRLMYLKKLKALAHPTKKVT LSLHREGKQINHKA VQRLMGT LSLKAAIKVKRYRSYRGEVGGT APNVLQRDFKATRPNEK WVTD VTEFAVNGRKL YLSPVIDLFNN EVISYLSERPVMNMVENMLD QAFKKLNPHEHPVLHSDQG WQ YRMRRYQNILKEHGKQSMR KGNCLDNVVECFGLKSECF YLDEFSNISELKDAVTEYIEYYN SRRISLKLKGLTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRREIE SII EAGRVSDDEIAKLGDNVE AWYRARLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFTRTL SVTDNMLTKLG MAGDVQKALEERNIFSVIDGT QPNPTTENVAAGLKLKENNC DSVISLGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIINTTAGTASEMTRFCIITDE ARHIKMAIVDKHVTPLLSVND SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	A	29246	1	375	
29072	59440	B	29247	1	5082	
29073	59441	A	29248	119	343	RMPKRRRWGKLSTIRCSTTCKK RLT*IVLPVRTPGRLCSSLKSVP ASHCLASCKAYS NKPWKRQPS KRHYVTMR

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29047	59415	A	29222	3	29	MQTEQQR/AVTRLCIQCGFLFLL QHGAESALVDELSSRLGRALG MDSVESSISNAIVLTTIKD/GQC LTSTRKNHDRGINMHVVTEVQ HIVI/LAEHHLDPPEP*EQQRR
29048	59416	A	29223	5	307	
29049	59417	A	29224	5	948	
29050	59418	B	29225	1	696	
29051	59419	A	29226	1	1083	
29052	59420	A	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*AAVKKRISEIIHENRGRY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	A	29229	1	2907	
29055	59423	A	29230	1	2541	
29056	59424	A	29231	1	1566	
29057	59425	A	29232	3	601	
29058	59426	A	29233	1	1347	
29059	59427	A	29234	940	1326	
29060	59428	A	29235	1	2547	
29061	59429	A	29236	527	1383	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	A	29239	1135	2067	
29065	59433	A	29240	1	1566	

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29037	59405	A	29212	514	1136	ILRIMQRGMKQFAGLLRLSGIK MLPSA**LGELLHAAGSFFQRG CLLFSTGGKIGVARRNFTGTGI DGI*TFADMSDGVSRALHM* NALRQVAHFTAPVNGQGIRQV TTGDFANVSNNFCQRSKQHTA NAVPRHQQNQYHHQRDNRLP LGKSVIICVVSDDIAIQFFTAEG VLSKRFAHCLMPSLGGLSKIGP SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041	59409	A	29216	1	1881	
29042	59410	A	29217	1532	2160	KHWSDSIPGTEADWSASTTSGC AGFAAFACSSS*VICLLSGAVA AYAPQLRHQAIRKVIIRRTSAFP LMD*TWSFLSSTNGLASCASIS SAGSGAGSASGVTKVSVDTAS GWPIFVTDRLSSCSTRFTLPGAN RLITVEPSLKRPISWPFSSATEPS FSPAGQVQRLMIPSRGGVMVP AQTVSMPLPTIVAPTGPYSSHLL GSFTLSPP
29043	59411	A	29218	1	1713	
29044	59412	A	29219	2159	2715	TIPAKPVPSMVASGTVRFGLTI PVLTAADSTPTKAHRQSRILLMI A*PSVVS AVFLAA*VAASNQC OPTIAVITTGIRTSTRPIVA/CITG FVTGAVEIVLVANSVIDISVGSP FSIPQMFSARLGIAATMAICPIMV SFSVAAINSASHNRQGFALQFFF NDAACGSGEFRILMQEEHPDSV VFC
29045	59413	A	29220	2	102	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM SVDLCHRDFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGV IGGAGSLAFPLPALIWCAVRYT PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNLRARR
29046	59414	A	29221	1	1464	

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29031	59399	A	29206	1782	3667	HRRRCRHGYVPVAYRCRIWKC GQFHPTGIAGCGRTGHRRLPW* RRLSAEQTWRTFYGALCAERQ RPGGP*RG\SRSIMIEIREGRGCD GPWGPHAKLKL D HLGKEVLES RLPGILELSRTFAHVDPSRFRLS HLSLHDGRYS D QSYRYNDTRD MVPINGSIHRIGREPHYHYQRG QQYIGLCRNCNVIDTHICIYLV D QPIMDDIRLLLLYSEISSAIIWLL PVVQGEHYMLVD P D TNEREER GRSETRGFPRVPLGRTVSTV.WY PLSNAATLAATRCRSRPHAF AE PSSNNGFITATPLGRTHFLGMA FPPSACWRLRAEPERVEAVLS ASGMNKAMRCGVSLICNFRLD YAPIEKQWDLHFADYFAEDLK LLAPLAKDGLVDVDEKGIQVT AKGRIRRLRRIRHLSMMPDAAL VASYQAYDFLRIRHKQRASAK QPNHCGTQHGSNGSLRTLWNSI DSGSVLTWCASLIFSSRKSLSPI QLVRSVDRGDVKKRYSMREFS LGETHSEAEFRELLEQNPSFVFF KPQSFAPVKGASAVPLVGRASV ASDRSIIPPGTLLAEVPLLDNN GKFNGQYELRLMVALDVGGAI KGQHFDIYQGIGPEAGHRAGW YNHYGRVWVLKTAPGA
29032	59400	A	29207	1351	1806	VIVGITSNSVTVA AVSSWCRTW VPVSVLCLNCYPASMALVRGVI RGV*TCLSLCPNCAAIFIFAFGA VIFCITSVGFLFPPMVYKSGLRF FVFT*MRDTGVPQRLRAPRRSL SAKLGPA CPFAYIVPHI WCRWI GWGTCVCLAICVCVCVAD
29033	59401	A	29208	1308	1647	RSWEVSIVEFYVVRPTGHV*HA SGNLSHHRKRHPLADQAARKG ETVPPRGRRS\WRTQAHP*HLR QHRGQHPASLPTRTGTPQPGRR AIYRIPVRTAGQFQRIE V GDFQR VGHQ
29034	59402	A	29209	1	2184	
29035	59403	B	29210	81	1356	
29036	59404	A	29211	1	2349	



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29021	59389	A	29196	21	432	GPGCNGVHRLCTE\QRDVRGTV RIVLKTFFNNCRDVTVFVAFEVNN TVSLLVATTDMTSGDTAIVVTT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFFNFPFNYQG VNDFDFDFKQFLHSSFDFCFGR VFSNFE
29022	59390	C	29197	1	1743	
29023	59391	A	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVPVLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	A	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSYGP LLSVRLLSHAWPNSLCPQLHCF LPGAIWSASSLLKSGNRPLIRLA SIVLPVPGGPISKRLCPPAAV/HF QSSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAVG FAATFAASIFHYVGVGPNRAD EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMHQPLGGYQGGAT DIEIHAREILKVGRMNELMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHR
29030	59398	A	29205	948	1620	

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29002	59370	A	29177	2268	2684	RCRRCKRRLRRFRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRHCHCG*RQC SSDGRKITSVHRGRNADGRELT HQA VRLLAYLSDRFARHHRHL RNAHRRGPDRIKERHFPA TKL RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	A	29180	3	126	
29006	59374	A	29181	1	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHK NPQSRGPISCQ*IQQ
29008	59376	A	29183	1	846	
29009	59377	A	29184	90	411	
29010	59378	A	29185	1	1580	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGV SADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK AAEIPRSTFYHYHLKALSKPKDY ADVKKRISEIYHENRGYGYRR VTLSLHREGKQINHKAVQRLM GTLSLKA AIVKRYRSYRGEVG QTAPNVLQRDFKATRPNEKWV TDVTEFAVNGRKLYLSPVIDLF NNEVISYSLSERPVMNMVENM LDQAFKKLNPHEHPVLHSDQG WQYRMRRYQNILKEHGKQSM SRKGNCLDNAVVECLFGTLKS ECFYLDEFSNISELKDAVTEYIE YYNSRRISLKLKDLASCLTVQ LFGVSTVMGLLIRILGSIFQKAL NISKIESFVAVTTIFLGQNEIPAI VKRFMIAESHEVLPHLYGMGH CGSRRWYAEWRPLHRVHEPSG
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	A	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	A	29195	1369	1743	

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28986	59354	A	29161	2	501	
28987	59355	A	29162	1	1347	
28988	59356	A	29163	3	2461	
28989	59357	A	29164	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVL PQGC DPHMESLI
28990	59358	A	29165	1135	2067	
28991	59359	A	29166	1	1364	MAGNRRFMCTPKTHGLSISQH GTFPEHAGCKIRCAGRSRVRP AELLAPYTGDI A AEGISKAMRG GAKFLHHGIKRQQRVVAEITE EWRMAPGP LEVAWFAGVIYHL YYRARRFFCAAQPLVSGFHEAE LSLDDAKWVLHPGPDAGFHVF DVDGRFVLAWMLFQGSYLAG ALGDQPVHIHLGQLLALWRPL QITQLIEVMLVGRGGDQAVGQ ATLGIDTNGGLYAKGPLIAFLG LMHLRIALLFVLGRTGCAYDG GRPQLAEKLYSELRAQGIEVLL DDRKERPGVMFADMELIGIPHT IVLGDRNLDNDIEYKYRRNGE KQLIKTGDIVEYLNAALLIAVT VLTSMEASDLVDLGMTLSPAD YAERLAALTQKCGLDGVCVCSA QEA VRFKQVFGQEFKL VTPGIR PQGSEAGDQRRIMTPEQALSAG VDYMVIGRPVTQSVDPAQTLK AINASLQRSA*CRDAGTLRLRA WLC*FLQRRYHRYKGPAVPQV ELCQICQRNEFCTQRVPGMCHV
28992	59360	A	29167	627	854	NAGDRNRNP SCTAARQYG*S RFYNCRR*RHGRKNLSAERNGL PEYRNCNPDHRPSVFLAAGRCF APTMCHDASE
28993	59361	A	29168	1	1593	
28994	59362	B	29169	1	3789	
28995	59363	A	29170	940	1326	
28996	59364	A	29171	1	1377	
28997	59365	A	29172	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRI LRPSRSARRCP SA PRSRQRRRSGPLPEAPRV S*Q IFPSQYWRYRQSTENQKQRLDP RGQIVNVPARRIIRQKRCKCKV AGSA
28999	59367	A	29174	1	1284	
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28978	59346	A	29153	1	1308	MMPLIDLEDPRLLVRREIGMLL HVDYLDLVHEKVTCRGRNGGQ DREKTTMEKVRSSGTICPQAPE VVNHYFTTDDGYRIISARFGVP RTQVRTWVALYEKHGEKGLIP KPKGVSADPELRIKVVKAVIEQ HMSLNQAAAHFMLAGSGSVAR WLKVYEERGEAGLRALKIGTK RNIAISVDPEKAASALELSKDRR IEDLERQVRFLETRLMYLKELK ALAHPTKKVTLSLHREGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGQTAPNVLQRDFKA TRPNEKWVTDVTEFAVNGRKL YLSPVIDLFNNEVISYLSERP MNMVENMLDQAFKKLNPHEH PVLHSDQGWQYRMRRYQNILK EHGIKQSMSRKGNCLDNAVVE CFFGTLKSECFYLDEFSNISELK DAVTEYIEYYNSRRISLKLKGL
28979	59347	A	29154	1	836	
28980	59348	A	29155	1	1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSLLRICSGVSPRS IPRWFTSVSLPSSFIRJITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSLS/VGSRPSGLRAFSSD CSPLPRTCSSLRRRVLMITTSRS *SLTYGVDPSVRPVLAAASEYF SRRYAGFQNPNNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSICTSTGGNTTL PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSIQSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCCKTKVVSGEYTVSSTMTLT DAEIAEGY
28983	59351	A	29158	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPPQGW
28984	59352	A	29159	3	601	
28985	59353	A	29160	415	549	

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28970	59338	A	29145	1	469	
28971	59339	A	29146	780	1052	
28972	59340	A	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	A	29149	1	1083	
28975	59343	A	29150	527	3213	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIQ/RPVMNMVENMLDQ AFKKNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADV RVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGYAVVALIKPGAQIGR SPVNCDVASCHVISFNLRLVELAI MRLLCRIA VLM SYRIEQRLMF LERLRHVGLIAHPAKKA IKKTR KPGMKVTFEQLKAAFNRVLISR GVDSETADACAEMFARTTESG VYSHGVNRFPRFIQQLENGDIIP DAQPKRITSLGAIEQWDAQRSI GNLTAKKMDRAIELAADHGI GLLRLAGGGKRLYWHLLDQLH RRNDNISLDLGNNAEAVILRED MLPRENFRPGDRVRGVLYSVRP EARGAQLFVTRSKPEMLIELFRI EVPEIGEEVIEIKAAARDPGSRA KIAVKTNDKRIDPPTQHEDEED EGLYDDPFPLNECSVGPGRHR FAPPEAQFRRPETLKGAPTSRIP ETSVGVSAGSDFEPHLMRELTC RLTALTWCYPGSAYAVHQPDE
28976	59344	A	29151	1	812	
28977	59345	A	29152	1	1830	

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28957	59325	A	29132	1	1114	MAEACNIGLEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLPPVDLTELLE IDAQTGFTEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK TINSGSNRKYFGSGRGITWYNF VSDQYSGFHGIVVPGTLRDSNF VLEGLLEQQTGLNP/D*NHDRH LRLSGETGRATHASSK*SDQTA TPTGRFNGTVTEIDAQTGFTE FAHVSESGARAQDLHISLRLRY* WLKPVIS/ALEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTGCGLEKQEEPPS LLRLNNRIKQLPPVDLTELLE IDAQTGFTEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960	59328	B	29135	1	1413	
28961	59329	A	29136	1	1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNLALL RRFHEATAQNAPDVVVWGS PMREFLHVDDMAAASIHVMEL AHEVWLENTQPMLSHINVTG VDCTIRELAQTIAKVVGKGRV VFDASKPDGTPRKLLDVT LHQLGWYHEISLEAGLASTYQW FLENQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	C	29144	1	2214	

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28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AGVAGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPRILIPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	B	29128	1	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQPMPTKGR\QARGAG \EVDVDWLIAERPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFRALISTA SALAGLILLCLFGPALLAGYTE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVLLVFILPFS LRRVGHAHH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	1	1677	

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28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQIL VEAATDIAKELYLGAVVDRSSR RVVFMASTEGGVEIEKVAEETP HLIHKVALDPLTGPMYPYQGREL AFKLGLEGKLVQQFTKIFMGLA TIFLERDLALIEINPLVITKQGDL ICLDGKLGADGNELFRSLILRE MRDQSQEADPREAQAAQWELN YVALDGNIGCMVNGAGLAMG TMDIVKLHGGEPAFLDVGGG ATKERVTEAFNPPGYIGPYQGV PPAGPGVTRMGKSVRRIVQVG CQVAAGSH
28941	59309	A	29116	1825	3186	
28942	59310	A	29117	366	1903	
28943	59311	A	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIAF CLHALLP
28945	59313	B	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	A	29122	1	783	
28948	59316	A	29123	96	215	
28949	59317	A	29124	1	292	MWWGGLLYWLAALVTLLWA ASQIQALKKLTCAISQTLEEQPV LNSKSWLTSLQNDYSLPDSLTE RIWLTLISQRISRGELREF*TGRR KLVTEQCLV
28950	59318	A	29125	3	529	
28951	59319	A	29126	1	884	MVDSLIRVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTAFGRRVSGVIEI GDGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLLRMKVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGVSIKFIDDGISTDGEM VLDKLARGYADLSKAESQWDE MMRTAGSLKLGTHASELIRSL LKSSRPSGLAQAIMVGRVNKT LYLLNYIDDEDYRRRILTQLNR GEGRHAVARAICYGQRGEIRKR YREGQEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEII DEDIARLSPLMHGHINMLGHYT FTLPEDILKGELR*RHLPPSSSA SPALPIGIHVHKHLLGDNRYPI WIMQPSAHHPARQPEHDNHFR



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28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALAL PGNCPVAHAQKRHSAPGTLSPD ARNEKQPLYG\GAAPETPNPRL PPLDSGILGGYIAPDNLITLSV GHSLFDERFGLAPQMPKKLQK MTRFPNDSLDAALCHGDVLLQI CANTQDTVIHALRDIHKHTPDLL SVRWKREGFISDHAARSKGKET PINLLGFKDGTANPDSQNDKLM QKV VVVTADQQEPAWTIGGSY QAVRLNQFRSVMN
28930	59298	B	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	A	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLQRLQEH FTVHQVANLSPQTVEQNAAIFA EAEGLLGSNENVNAALLEKMP KL RATSTISVGYDNFDVDALTA RKILLMHTPTVLTETVADTLMA LVLSTARRVVEVAERVKAGEW TASIGPDWYGTDVHHKTLGIVG MGRIGMALAQRAHFGFNMPI/R L*RAPPP*RSRRTLQRPLLRFY SVTRVRFRLPDPAVN**DASSV WRR TIRGPSLGLSPGWNTRVSL CAFFG
28934	59302	B	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	A	29111	1	777	
28937	59305	A	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN FC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMRYHY SQLKCEMNVG VYLPPKAANE KLPVLYWLSGLTCNEQNFITKS GMQRYAAEHNIIVVAPDTS PRG SHVADADRYDLGQGAGFY LNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALVLALRNPDEYVSVSASFSP IVSPSQVPWGQQAFAAYLAEN KDAWLDYDPVSLISQGQ/LRCG NHG*SGVE**FLRRQLRLQI*KD WPQ*EAHVH

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28924	59292	A	29099	1	1567	MKLNKAGFNVPEYSLLKMPP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCS TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDVVAHDSRSIQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLERKDLALNQAMIPLGSCT MKLNAAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDA\VCMQPNSSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIAIEKMGVPIKCTTEV G\NTLTLEQVKAENRAVLTVG LSSGSGPLPFEHSDVEI\VDLQ RARQAQGDISIPQSALIIGGGDV AMDVASTLKVLCQAVTCVAR EELDEFPASEKEFTSARELGVSII DGFTPVAVEGNKVTFKHGDRL TAPFLGVADKRNKSAGNHP
28925	59293	A	29100	107	892	LAICTGTYSGRQVLPRFVDRGA SLIAEERNAGARRRAGIRTTSA GGGLCAYAIVEF*CWRNCARFE LN/AGISVPI/SEFIGATMQQTVH AEQSAISHAWLSGEKALAAITV NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP KDLEIKTLLMDEQDHGYALTG DALSQAAIAAANRSHMPYSKSP SGVALECKDGRIFSSEYAENAA FNPTPDIQRAVLAEKADAPLIQ WDATSA TLKALGCHSIDRVLL
28926	59294	A	29101	1	3100	
28927	59295	A	29102	1878	2699	GTARNLTVSLSYSSSGTPSNA PNARMEELGPHPGEASSLFHPE SPLLDELFLPEYKAGRTPNPDI GHYVRRADVVDGKSRLRLGLDS NKDQSYFLYTLSHEQIAQSLFP VGELEKPQVRKIAEDLGLVTAK KKDSTGICFIGERKFREFLGRYL PAQPGKIITVDGDEIGE HQGLM YHTLGQRKGLGIGGTKEGTEEP WYVVVDKDVENNILVVAQGHE HPRLMSVGLIAQQLHWVDREP FTGTMRCTVKTRYRQTISLGPL RKPPHNRCLEI
28928	59296	A	29103	358	1160	

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28919	59287	A	29094	1	725	MHPRFQTAFQALADNLQSALE PILADKYFPALLTGEQVSSLKSA TGLDEDALAFALLPLAAACART PLSNFNVGAIARGASRRSAKNIP RAVRQVFWRILLFYVFAILIISLI IPYTDPSLLRNDVKDISVSPFTL VFQHAGLLSAAAVMNAVILTA VLSAGNSGMYASTRMLYTLAC DGKAPRIFAKLSRGGVPRNALY ATTVIAGLCFLTSMFGNQTVYL WLLNTSGMTGFIAWLGIAISHY RFRRGYVLQGHINDLPYRSGF FPLGPFAFILCLIITLQNYEAF LKDTIDWGGVAGTYIASGGEP VNSHAFGVLRNVVSIAVFFHQF GDAIKRLFPTDLLPFIRTWRTVF RKLQTAFGVDEIHQASAFRTKC TAVDRVIRIAFDMDRLDFFSWR SGYISRIPLIGLYFACALERHQN ERQPIILLSDQNAIATINQLAIER DVLNCRVIIARSLSELVAIREEIE PLLIINNSHYLLDDAVNNYITVK NIITAAGIEQIKHFLATAFIRQQP ERFFSAPGSFHYSNVRGESWQH ITRQICQLVAQHHTADEAQRI IAREGEGENLIVNRLAIPHCWSE QERRFR*TVAWWRAA*CAVCD DGDGCRSVLPDLHVWQPDGIPV AAEHLRDDGFRYLAGDCH
28920	59288	A	29095	3	453	
28921	59289	B	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ QATFTL*QLALFAIEPGLMTDP DIQVRGTTLPYGRGAHGVYT SNWKLTFRRILY
28923	59291	A	29098	1	2862	

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28904	59272	A	29079	1886	2329	PLL VWINTRPSLT TGRESASPAT LVCHATVPSLVIASHVLSFL*W SFTVLVISRIGVAFAHAFWSIT ASLAIRMAPAGKRAQALS LIAT GTALAMVLGLPLGRIVGQYFG WRMTFFAIGALITLLCLIKLL PLLRRTVKY TSGC
28905	59273	A	29080	1	2319	
28906	59274	A	29081	3	194	STSSLAAQSLRFGYETSQTGLA TYCGEKIQ*FFADLQQPVCADS YPLL VQMKKLGPIVFFFDI
28907	59275	A	29082	3109	3384	
28908	59276	A	29083	703	1000	DCFLRRLIKRPFGTSMKDQAVR FEEGFMAMGALGLAMVGMTA LAPVLAHVLPV IIPVYEMLGA NPSMFAGTLLA\WIWAAVFLAK ELAGGVRL LVLI F
28909	59277	A	29084	2040	4603	
28910	59278	A	29085	3	94	
28911	59279	A	29086	3	148	YAEHMLEVMSSIGDYT/NPRPA SRPVTKFDQRGHR LGHGVWNL MFERVK
28912	59280	A	29087	27	227	
28913	59281	A	29088	344	1067	
28914	59282	A	29089	798	1049	
28915	59283	A	29090	1	1473	
28916	59284	A	29091	1	720	
28917	59285	A	29092	45	208	
28918	59286	A	29093	1	2499	

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28889	59257	A	29064	498	707	
28890	59258	A	29065	510	554	
28891	59259	A	29066	600	734	PECLSAPDH*YKHCCSTGTQAR QPDADCPLLPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD LWPGEVLGIVGESGSGKTLLK SISARLTPQQGEIHYENRSLYA MSEADRRRLRTEWGVVHQHP LDGLRRQVSAGGNIGERLMAT GARHYGDIRATAQKWLEEVEIP ANRIDDLPTTFSGGMQQRQLQIA RNLVTHPKLVFMDEPTGGLDV SVQARLLDLLRGLVVELNLAV VIVTSSPDQDWGFTPEPRLAAR FPGSTHSSRSRRNRGRHPRPRS LPTPSAPHSRAPGDGVKLVPPP ARVTRNEPAPSDSVTLGVPHEP GACIGTPILTFVRPSTSAINAAA EESTGTILFGAGGFKRTDLNDT ESDSTTLVASRYWDLSSGWQR AINLRWSLDHFTQGEITNTTML FYPGVMISRTRSRGGLMPTWG DSQRYSIDYSNTAWGSDVDFSV FQAQNVWIRTLYDRHRFVTRG TLGWIETGDFDKVPPDL*LKSR VGQRSELGSQYTPRARVEPPKL LSRKVRAHFGSRAPGAGRA*RH LRAPDCGVRVWVWAGSGAGDG GGRGCGSGTSEWILGSGRRGE
28893	59261	A	29068	84	128	
28894	59262	A	29069	1547	1822	CSRCSIPAFRVKPAPLKPRVFSP AWNUPERLWHLAPSTFSGGEQ QRVNIAR/ELYRRLPHSAA*RN YRLP*RQNSAALSRLYAAFLPR PQYHH
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	A	29077	1428	1619	YAARRRALCGSPCFPGGCNGE NCRLPPQLHADLTARIFYETRG WWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG* HQLWARWQNNGLAHTPRADS THQQSALDGRISLT

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28882	59250	A	29057	2	1760	KSQLHDPCCAPIQQEAVRAVV GPPQQLHGFVVERGVQCQREC DFEKELEARIASLSDSVSNAREE RMALRQEQEQQLQSRISLMQR APVWLAAQNSLNQLSEQCGEE FTSSQRTTHGHSEGNITKRGLLG ELRFENGDPNDQSYGRHKDG MAEIGTFHGGDLRGLTNKLDY LQQLGVNALWISAPFEQIHGW VGGGTKGDFPHYAYHGYTTQ DWTNEDANMGNEADLRTLVD SAHQRGIRILFDVVMNHTGYAT LADMQEYQFGALYLSGDEVKK SLGERWSDWKPAAGQTWHSFN DYINFSDKTGWKWWGKNWI RTDIGDYDNPGFDDLTMSLAFL PDIKTESTTASGLPVFYKNKMD THAKAIDGYTPRDYLTHWLNQ WVRDYGID/GFRVDTPKCLRCN PSITIGTNYSAS*PQWSSIPGAL* G*/PAWAG/GLPWAPSVLLLDH LRQGFTMLEENLGNTIQDIGMG KDFMSKTPKATVTKAKIEKWN LIKLSFCTAKETTIRVNRQPT WEKIFAIYSSDKGLISRIYKELK QIYKEKNKQPHQQVGEQHEQT LLKRRHGCSSQTHEKMLNHQ
28883	59251	A	29058	1	1119	
28884	59252	A	29059	3	2599	
28885	59253	A	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG NAAGDP*YQMGPHHRGCGKP VPLPDHQSENLRWW*RRAWCG SGGYR\MAEGRHAAQGIIDWLG LDVDKLGAEERRKVLQVKTE NLQAERNRSKSGQAKARGED IEPLRLEVNLGEELDAAKAE DALQAEIRDIALTIPNLPADEVP VGKDENDNVEVSRWGTPREFD FEVRDHVTLGEMHSGLDFAAA VKLTGSRFVVMKGQIARMHRA LSQFMLDLHTEQHGYSYENYVP YLVNQDTLYGVGLYPLGALAS GWLPRRERKDATPGPTGYPG AHGNLELPERSEGPRAGGEPRR RTGHTQKGSPPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	A	29062	1	2530	
28888	59256	A	29063	675	920	RTYRLAGRQKQRRGGGTDSRS QNPWRSHRRHLP*RSSGAGKR GGKRFAGGAERRNPRLCRKPEP PAGGDGRRRRLLAAAGAD

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28866	59234	A	29041	1	1339	MTGKCGKFGNFLESWRAQKTG ICGKVVNFLENLLNGFGQNAY SDTDNEVQAEVVSDDKDELVG NWSKGHSCYAKRLAFCPCLR DLWNFELERDDLGYLVEEISKQ QTIQEEADHKNLESLQTEDAIE KKTPFSGEKFKLAAEICISNKDP NINSQDDGENVPRVAVHPNGC FAWKLPVLSRKFERKPIYWILS EVAKRLGPDVYQKFTGRTQE QWLQHLAYAKMEAKDPALPSY DELKKMGIYKRKDPNGHFVAY KAFRDDPEANPLKTPSGKIEIYS SRLAEIARTWELEKDEVISPLPV YASTFEGWNSPERRTFPLQLFG FHDKSRTHTSTYGNIDLLKAACR QEVWINPIDAQKRGIANGDMP YVFSSQMAKFTPRTGLSSLIWK AHKCGEALETQKQ* <sup>C</sup> * <sup>Q</sup> SGAT LPAGPRARAWPPYPRLFPTGLA CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCPLPGTVSV* <sup>S</sup> GL YVRGAQHGRYQ* <sup>H</sup> HRCCTSDK IWRADKG
28868	59236	B	29043	1	1617	
28869	59237	A	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	A	29046	444	3793	
28872	59240	A	29047	475	732	
28873	59241	A	29048	1	219	
28874	59242	A	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	A	29052	172	378	LSLLRELGPVVAALLFAGRAGS ALT/VRNRPDARYRATLQYGD DGGGSAASGYFSPFLGWGYFIT TVDG
28878	59246	B	29053	1	1641	
28879	59247	A	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	A	29056	1	1500	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTTL AEGLLAAEEAGIPLVVNHVGG MFGIFFTDAESVTCYQDVMAC D/GGTL*AFLPYDAGRRCLQHG RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRRDR QGRIHNLNDRRRHWHRVRVCH LLRRERSRKDAPADGHPPLARA VGGRNQNF*FGELRTTTCFTQTD FLTFLNLTSVTSNEASFTQFRTQG LVVFHQSAAGDVTDRSLTRDT TTFNGDVQVQFLNHVDQFQRL TNYHAGSFTTEVLFRQLVDYD FTVARFDENASCGTFAATSAAV LIFSHCLRLLCRVVVLVTRVNF QFTEHSTTQRAFWQHAFNRDF NHTLRTASNHLFKGRLFDTTDV AGVVIVHFVSTLVAGYSNFVSV QNDDVITGIYVRSVFRFVLTAQ ATSQFSSQTAQSFTGRVNNIPV AFYGFWFSCAKYYRHGARWCS NGRKIDQRHHCFFCPCIRTDFA VEIGKEEFIT
28861	59229	A	29036	1	797	MIVFIENFKTSSPKYADILLPDL MTVEQEDIIPNDYAGNMGYLIF LQPVTSEKFERKPIYWILSEVAK RLGPDVYQKFTEGRTQEQLQ HLYAKMLAKDPALPSYDELKK MGIYKRKDPNGHFVAYKAFRD DPEANPLKTPSGKIEIYSSRLAEI ARTWELEKDEVISPLPVYASTF EGWNSPERRTFPLQLFGFHYKS RTHSTYGNIDLLKAACRQEVWI NPIDAQKRGIANGDMVRVFNH RGEVRLPAKVTPHPVGTWTAE
28862	59230	A	29037	1	1019	
28863	59231	B	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	



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28846	59214	A	29021	878	1267	LNSWLPSVPTV*SSVFNAL*TG* ISPAFNPFAADM*SASGLP*IKSPL STSTLFFTSRLASLIRLAVRTSPN FSVA VSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARSVALN RFLIKSTGNACK
28847	59215	A	29022	294	2305	
28848	59216	A	29023	5	337	GAPQHQQMMSTYRINGRESPML TYPSTPNFFWLAWQARDFMSK KYGRRFPARFLWRSTPAPGVR KTIFIFISLVFVLMCANSWITI RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSRHLQLSFFPKID LLISVGDNIDRGPESLDVLRLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLAVIWI GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLEG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTVSVDKVVVEKK GTKEVAEAYLKLYLSPEGQEIA AKNYRPRDAEVAKKYENAFP KLKLFTIDEEFGGWTKAQKEHF ANGVIAVVAAGIGYWKLGTGEE SDTLRKIVLEECLTNQQNQNP SPCAEVKPNAGYVVLKDLSGPL PYLLMPTYRINGTESPLLDTPST PNFFWLAWQARDFMSKKYGR RFPIARFLWRSTPAPGVRKTIFIF ISLVFVLMCANSWITIWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPLLPLSPLSSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQLVATAR WFARA*ILHPL
28851	59219	A	29026	1936	2490	
28852	59220	A	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	A	29030	3338	3553	
28856	59224	A	29031	95	1289	
28857	59225	A	29032	1	732	
28858	59226	A	29033	1	672	

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28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK SDRAVHQGHIPRQFY*SLRRNL TNRHIQLAIGGAIGTGLFMGSG KTISLAGPSIIFVYMIIGFMLFFV MRAMGELLNLEYSKSFSDFAS DLLGPWAGYFTGWTYWFCWV VTGMADVVAITAYAQFWFPDL SDWVASLAVIVLLLTNLATVK NVGEMEFWFAMIKIVRPLSGSR TKKMSKSDNRRNNVIGLLEDP KSVVKKIKRAVTDSDPEPPVVRY DVQRPKRSALLERAPERFQEVF ILKGREDKRLPLIHAIHESQGG GYPVGKPPISRREKRPCRASGA YSPPVLLILMDPLGNLPIFMSV LKHTEPKRRRAIMVRELLIAL VMLVFLFAGEKILAFSLRAET VSISGGIILFLIAIKMIFPSASGNS SGLPAGEEPFIVPLAIPVAGPTI LATLMLLSHQYPNQMGHLVIA LLLA WGGTFVILLQSSFLRLL GEKRVNALERLMGLILVMMA
28839	59207	A	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	A	29016	38	457	LNRLCLKLVHASQSSRAMVFSSI RSFMFFSTLFILVRRQFSR*TIML SANSDSLTSLLPIWLLFISFSLT ALARTSSTVLKRSGESGHPCLV PVFRGNTFNFSFSLMLAVGGV LHCEINCRICSTGRSANPLDSCI
28842	59210	A	29017	899	991	
28843	59211	A	29018	1740	1868	
28844	59212	A	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA TCMEQFRPKTIPPLAIPERLNAH CEELYELIASLNNILNLYMPAG QEAHRFAMGELPDEVLEICQR LAKLTEMLRGLAELFLNDLSEK TGSHDIVRLHRLILQMNRLGML FEAQSKLWRLASLAQSSGAPVT KWATREEREGQLHLWFHCVGI RVSDQLERLLWRSIPHIIVTSAT LRSLNSFSRLQEMSGLKEKAGD RFVALDSPFNHCEQGGKIVIPRM RVEPSIDNEEQHIAEMAAFFRK QVESKKHLGMLVLFASGRAMQ RFLDYVTDRLMLLVQGDQPR YRLVELPANASPTVSAACWW AYSHLPKGLI*KVICSARCISTK SLFRPSTARW
28845	59213	A	29020	1	2022	

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28831	59199	A	29006	1	535	RPYVLPVAGSNALGAILGYVES ALEIAQQCEGAVNISSVVVASG SAGTHAGLAVGLEHLMPESELI GVTVSRSVADQLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEAVKLLARLEG ILLDPVYTGKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PHV
28832	59200	A	29007	1	1953	
28833	59201	A	29008	1	656	MKLMAIQEQARGEQCFRDSEW DLQFHIQVALATQNSALAAIVE KMWTQRSHNPYWKKLHEHIDS RTVDNWCDDHDQILKALIRKD PHAAKLAMWQHLENTKIMLFN ETSDDFEFNADRYLFAENPVAI AKELELTASAEILLWDDYFAPG YGVPNDEGMEAVKLLPRLEGIL LDPVYTGKAMRGLIDGISQKRF KDEGPILFIHTGGAPALFAYHP HV
28834	59202	A	29009	1172	1371	
28835	59203	A	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	A	29011	413	2798	
28837	59205	A	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAG FVFFSPRKALSGSKFTFLPT

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28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLRLAR AETTTAPSTPMKTHRVISMVFF TCSQTGTPSASPVKSSLKVSSLN IIIASTTNRPS/VQQF/WPVSPPG DGTRRYP\SISLTVLTGNDNVNL LRAGIDLAIFYDDAPSAQLTHH FLMDEEILPVCSPEYAQRHALT DTVINLCHCTLLHDRQAWSND SGTDEWHSWAQHYAVNLPTSS GIGFDRSDLAVIAAMNHIGVAM GRKRLVQKRLASGVYPPRCAY PRTHLLETSTTSGVNGVGTYS PFWRMLLNSFVMAFSITLGKIT VSMLSAFAIVWFRFLRNLF MIFITLMLPVEVRIFPTVEVIAN LQMLDSYAGLTPLMASATAT FLFRQFFMTLPDELVEAARIDG ASPMRFFCDIVPLSKTNLAALF VITFIYGNQYLWPLLIITDVDL GTTVAGIKGMATGEGTTEWNS VMVAMLLTLIPPVIVLVLMQR AFVRGLVDNPAANYIHYGVRE SGMTAIAANGIAHHGGFVPYTAT FLMFVEYARNAARMAALMKA RQIMVYTHDSIGLGEDGPTHQA VEQLASRLTPNFSTWRPCDQV EAAVGWKLAVERNHNGPTALIL SRQNLAQVERTPDQVKEIARGG YVLKDSGGKPDIIILATGSEMEI TLQAAEKLAGEGRNVRVVS LPSTDIFDAQDEEYRESVLP SNVARVAVEAGIADYWKYVG
28827	59195	A	29002	2253	2546	
28828	59196	A	29003	279	629	NGAGHL*RPPVDGATAAPAGG RYAHLRVCPELPLWHLPAWRI YRSGS*SAPCHCRNHRSGSAWQ KHYGNRFRFRTVRPYRGRALH LRGRNTAITQAADWRLATAQL LEIAGVGDE
28829	59197	A	29004	313	638	RWRQRWFWCLHCLVLFRTIPR TFALSQCRPWDDSRSDTSM SHSIQWNRMYCNCMSQDEQ EADANGKGPAAQVGDRQAW AGRCRSHRREGTIPGNPHPR AS*RAGWQR
28830	59198	A	29005	1	1182	

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28808	59176	A	28983	361	738	FLQPFPPKREINKFIRDIANNMK TDFFSAVTLFTDCVTVMLWII*F FQRKFLLKGFIPPLGSFYRE*IIT SLFLYLLCNIFLATHRISCDDFSF NIQHVKKFWDSNLIIRFLIRLDL SDDQTVHC
28809	59177	B	28984	1	1263	
28810	59178	A	28985	363	569	KGYSRRSGKHRQGCCNVLRRL FPDHQTAPRPMPLKRQTRAPGQ SPPGLPADPHPGQF*LPLLGRF AR
28811	59179	A	28986	1	1035	
28812	59180	A	28987	275	721	LMVSGFLTSPKDDHERIMSGEAR AILIASNSSVLVCAFRNFNKSFT DLLPSELAQSASERISFNNTLKD SGMPGSI*WLPSTMFLYILVRPF TSSDLTVSISCRVYAAPYASSA HTSISPKR*PPNTQRLLTGPVGT FWGRKPPLFPTP
28813	59181	B	28988	1	2082	
28814	59182	A	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	A	28991	1	777	
28817	59185	A	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYGSRGAGKCRESERL GESRNPGSIGLENELTAEDVAS ADMVILTKDIGIKFEERFAGKTI VRVNISDAEFLMTNRISRLKTA LFANTREISLERALLYTASHRQT EGEPVILRRAKATAYILEHVEISI RDEELIAGNRTV/ITARRDYVA GNGPLLAERAGSIPDASAGPL CYQRRRL
28819	59187	B	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLAAVAIREINHDSGSATF RTPRDPRTVAGKYNLGASLYK SELLA*LHSAGAGCLSCQRAKL GLGRRR
28821	59189	A	28996	1	2115	
28822	59190	A	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPSASLI STNKSPLDDVE*RSLISKAPGDT
28824	59192	A	28999	147	1456	
28825	59193	A	29000	1	439	

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28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHA F*PLLGDFGCRNGVIQGRENAH LMNGGGRRVTALHFQQYRFHH LFNILTARHHLIDNANHAQIDR* RFAFMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	A	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	A	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	A	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFGHQLIAGDHFF HHFQAHLVQFGGDFQFLNLG EGQLVVSIFTPVRLAVHGVKIE TVFVGFSLSIHGSQTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLPRVHGATAPSCASQFL VFAAPTTPRDRHG*RTDDSTPQ RLSSPAVEKAPTASSASGNSRN DKPLREITLITSDRPVPDAAVSP TGFWPLTIPFHRCRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FWH RFHGHGFPAGGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	A	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGVEVGTV QDISLSDDLRLKIEVKVSIKSDMK DALREETQFWLVTPKASLAGV SGLDALVGGNYIGMMPGKGKE QDHFVALDTQPKYRLDNGDLM IHLQAPDLGSLNSGSLVYFRKIP VGKVYDYAINPNKQGVVIDVLI ERRFTDLVKKGSRFWNVSGVD ANVSISGAKVKLESAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	A	28980	1	612	
28806	59174	A	28981	128	1742	
28807	59175	A	28982	1	2688	

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28775	59143	A	28950	34	437	CGRLLQKSGFVSVGIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGDTDQ/D ARKRERFPLRG*SPAIEQSPPAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRPHHRERRLP
28776	59144	A	28951	1	457	
28777	59145	A	28952	176	757	KPMKSTAAAADAALLSAVERQ VIDDAAAHLSEVAQGDDVDAI EQAIKNVDKQTQDFAARRMDQ SVRRADRSDLIETFDHVCTVIFI RDGITSAEVETADTARGNV DVI RTGEVGAVCGTEETKSILQYLQ YAITKDIFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSPPVSIRMMFGI
28778	59146	A	28953	1	1503	
28779	59147	A	28954	425	619	AGWSFLPSPA EQNRWRPPLSRF CQIPAPLQVRS*LACRFFAAYSP PLLRKSPAASMA YTTSSLH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAQVFKAHLRDDVHHHIDGQ VTATESVMEGNRH AVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLESGKIAFSATIPGRYPFLS LRLFNFLRHFDCLILRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	B	28957	12	271	
28783	59151	A	28958	309	1238	GSGSCYSALVKRKWSARSLRA DRNGARRGAYVGRKFGHFGPG LAGFFSAHASNLCRRSDRAPAH YHQLLN FADPVDMMQ*KRGM VFLLLMDQRQQRVDDWRRLPS LLSVWQSCGDSGRRAPGGR*FH WRFQATVFQALAE DLRRNLQI VVATVAF/GMGINKPNVRFVVH FD/IPRNIESYYQETGRAGR/DGL PAEAMLFYDPADMA/WLRRCL EEKPQGQLQD/IERHKLNAMGA FAEAQT/CRRLVLLNYFGEGRQ EP/CGNCDICLDPPKQYDG/STD AQIALSTIGRVNQR/FGMGYVV EVIRVAAFLEPDYSHRP
28784	59152	B	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	B	28962	145	494	

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28769	59137	A	28944	1	2539	MPIEEPALRSWQRPFLKWAGG KYSLPELDRIPAGKRLIEPFV GGGSVFLNSDKHERFLLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENYTLIREAFNAQ RLDAVERAAAFLYLNRHCFNG LIRYNLDVFFNVGFGKHKQMT NNEKSGPFEGLLVIDMTHVLNG PFGTQLLCNMGARVIKVEPPGH GDDTRTFGPYVDGQSLYYSFIN HGKESVVLDLKNDHDKSFGHT GPLKDAPAYDTIIQAMSGIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALYGREKSQRGAH VDIAMFDATLSFLEHGLMAYIA TGKSPQRLGNRHPYMAPFDVF NTQDKPITICCGNDKLFSALCQ ALELTEL VNDPRFSSNILRVQN QAILKQYIERTLKTQAAEVWFT PFSNKYNGHRIARTDKASMP TV YSESLFVEGIIRASTSMTTKQGP SLRTGRTLRLKFCPLSETAATDTS SIFPSKFTPTASRLPGFSFIRSPK MTQSVLLPPGPFTRRQAQAF TT TYSNITLEDQDQSHFRLVVRDT EGRMASVQTRPPADREAFTRI H LPEHTLYPHTPAIAAGVFIDGDI PMTTQTQHD LAPANQPEFELTV TPVPDEQRIDFWPQYFGAIPQW LLEPHIFAWMDRFCEGYSGGI WSFYTLNNGGAFMSPEPDNDET WRLFNCLNATMPPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	A	28946	1	3033	MVWGFCTCSTTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDLTQMMTSTLFSSPSV HNVMETVTQETAPPDEMTTSFP SSVTNTLMMTSKTITMTTSTDS TLGNTEETSTAGTESSTPVTS AV SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTRESQTSTL THRTTSTPSFSPSVHNVGTVSQ KTSPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVTGSLMP
28772	59140	A	28947	636	725	
28773	59141	A	28948	1	1123	
28774	59142	A	28949	2345	3644	



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28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	A	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	A	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVAALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGEE QISLGVRNTSPDVPYLIQSWVM TPDNKKSadFIITPPVFLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAVPSTTKRKEGNTLKIHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	A	28941	76	981	
28767	59135	A	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPAHQRQWSASYWRS *SSSFRLNKKCHTQNHsNCIKM ARE

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28747	59115	A	28922	3612	5412	PGLKHQNNGHRGPDAETKGVT RDFGPNAPLAG/VRLN/LERLR DTHHIDVAPLVARLDQMMESV SLLQLARAGQSFSNGYQHV KLEDVILPSYDELSTMLDQRQ QTLLLPESAADITVQGATLLR MLLRNLVENAHRYSPQGSNIMI KLQEDDGAVMAVEDEPGIDE SKCGELSKAFVRMDSRYGGIGL GLSIVSRITQLHHGQFFLQNRQE TSGTRAWVRLKKDQGA YPMSE KVVFSQLSRKFIDENDATPAEA QQVVYYSLAIGHHLGVDCLEA ALTCPWDEYLAWIATLEAGSE ARRKMEGVPKYGEIVIDINHVP MLANAFDKARAAQTSQQQEW STMLLSMLHDIHQENAIYLMG VFIMLIFFPAPVASEKPLSPDCW TTHTLRMIGENSGLVSYMREK AVSPNCWNVIHYSGLHLELLS SYDVDVNQIINTICEWISLIKTR GVRRPEFQTLLTGSGSEHGERFI MNRPTLFFTDLAHVDRFTQYV HDTAQRFTYRDFNRVFEVFI QTATQTVGGTHCDAPGWFWP GAVQSVPAALIAVAAAPGLA SFLPFARRVPRTVVALLAQAAA YADGMPARADGSFNPS
28748	59116	A	28923	1	2910	
28749	59117	A	28924	470	723	PGFGDARKLISLNFFIWV*TA*I M*P/LAGSDFVYRNS*RNVFIAQ TLQLRSRQPVTMHATRAFT EHNILIRFECCEYSRYLFT
28750	59118	A	28925	599	1117	
28751	59119	A	28926	279	455	SLSHSSGRCSRGGISFWVWVEF GPVACLAASVV*L*VSVVWLW LSPSGQGCLGCRVWL
28752	59120	A	28927	1	2913	
28753	59121	A	28928	1	2328	
28754	59122	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	A	28934	467	631	LEVIEAPQPNWS*SVQQSACST WPGCWVDLEDPOVWVWYEW TTKRASLLPIFQD*LKALRKAQ VWAFAS*STWPGCWVDLEDPO VWVWYEWTTKRASLLPIFQD
28760	59128	A	28935	989	3010	

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28739	59107	A	28914	1	333	MFQDPVAFDDVAVNFTQEEWA LLDISQRKLYKEVMLETFRNLT SVGKSWKDQNIIEYEQNPRRN FRSLIEKKVNEIKDDSHCGETFT QVPDDRLLNFQEKKASPEIKSCD SFVCGEVGLGNSSFNMNIRGDI GHKAYEYQEYGPCKCQPK KAFRYHPSFRTPQRDHTGEKPY ACKECGKTFISHSSIQRHVVMH SGDGPYKCKFCGKAHFCLSLYL IHERIHTGEKPYECKQCGKSFSY SATLRIHERHTTGEKPYECQQC GKAFHSPRCYRRHERIHTGEKA YQCKEKGKAFKTCQYVRIHERT HSRKKPYECTQCGKAL*YSLKS GSLMP*ALFFWLRIVLAMWAL LWFHMFNVFVFSNSVKKVIGS LMGMAWNLQITLGSMAIFMILI LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	A	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLLTPLLFSLLCF ACRKRRLSATRTVTVLHSLGIT LLLILALWVVQTAADAGEIFAA GLWLHIDGLGGLFLAILGVIGFL TGIYSIGYMRHEVAHGELSPVT LCDYYGFFHLFLFTMLLVVTSN NLIVMWAAIEATTLSSAFLVGI YGQRSSLEAAWKYIIICTVGVA FGLFGTVLVYANAASVCGTDH GGRMMRSWNGGQLISKLLAIT PDKLVLDGFSQAEDNIAVLKA QHISISAETQGAKVEFTVDQLQ QSEYLQLPAFITVPPPTLWVFQR RRYFRISAPLHPPYFCQTKLAD NSTLRFRLYDLSLGGMGALLET AKPAELQEGMRFAQIEVNMGQ WGVFHFDAQLISISERKVIDGK NETIPTRLSFRFLNVSPTVRQ LQRIIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	A	28918	518	1046	
28744	59112	A	28919	8	893	
28745	59113	B	28920	1	3129	
28746	59114	A	28921	1	1284	

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28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLISLGLWSCFSKGWVT TPTTLSCSPPPRRGRMAPWAW GRSRARMCWSWSWSTRPSRPC AVRWSWSSGATGSCWRRPVST APPRPPWRPAAPTPAPLWART RMPSHWPSTTAPAATAY*/DPD AGYQPTLAAPAEPSKYSLAS LDRGQGRGGGGGGALEYVPKA VSQPRRHSRPVPSGKYVVDNSR PPTDLEYDPLSNYSARHLRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSKPSCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPIKRSEA*AISTARVI PSGDSIAASRPVLPGRPQAFSIR RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903	1	2001	
28729	59097	A	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	A	28906	531	949	
28732	59100	A	28907	44	477	
28733	59101	A	28908	161	333	
28734	59102	A	28909	1	394	MEGVAFLTFLAARA AVGNRPA SPQIVRKQREGHGILTRDPVA FDDVAVNFTQEEWALLDISQR KLYKEVMLETfKNLTSVGKSW KDQNIIEYEQNPRRFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGPkPYKCQqPKNKKAfr YRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMSHWEKP YECSKCDKAFHSSSSYH
28735	59103	B	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPLKNIPSTKN*Q RRRNTSQR*LRHQPFSSASRPG SRLRFAIGPLQPAEAGMVT
28737	59105	A	28912	358	878	KLCHIACIHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGFPKL LTLIGVLSSVSPFMISKGSEGNG GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLTfIRSLYRVHYV CLCPFMNSKVLGRSEGFPFTLT CIGLLSIVCRFPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	A	28913	1382	1416	

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28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY* KNFAKKLI*GDIREKLQKLEGF AGMNATQLIEVATEVYINCDQE AKKETEQRLRKKANLLAAALT KRKINIVKGRECSHGCGHGRGQ VEQRAKRWLRLRGGWVKAFP VRTEKAREVTKVLLRDIIPGFG PLTLASDNGPAFIKIVQELTQL LKIKWKLHIAYWPQSSEKVEH MNQTLKQLKKKFCQETHLRWD QVLPMLLRVRYTPTKQTGYS PMRSCSANLK
28713	59081	A	28888	1	963	
28714	59082	A	28889	123	593	KRQVLAGFLITPRRLPKNWT WCWWSM/PAQVKQVLFGETG VAQHLKPGTAVMVSSTIASAD AQEIATALAGFDLEMLDAPVSG GAVKAANGEMTVMASGSDIAF ERLAPVLEAVAGKVYRIGAEPG QVRP*KLFTSC*RAYILLPEPKR WHLQPV
28715	59083	A	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT GLPRGPHGRAAGNPVDQQFAA GDLGLSPHADAHPGGTDDVRW CLIST*KRWDSGV*AGAGQYSG WRRRSLRWR
28717	59085	B	28892	1	2118	
28718	59086	A	28893	1084	8334	
28719	59087	A	28894	2029	3313	
28720	59088	A	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	
28724	59092	A	28899	1904	2281	CSAYAGLHPFWLKSTRFCTHIL APATAISPNTTIDAPPITAAGMV *ISAPNFGEKPNMAMTAAATN TSVE*TLVTAITPIFSA*VVTPLP PTEPESIVARPSPTNARPIYGSIL RPVIPATALR

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28700	59068	A	28875	65	436	REVWEHAKRMLGDSSLDMGM DDELYTMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRLPNQEHSL*ASVP ELKCAASWTKRKKNSTFIASSA IRLTLTWKPKPFLSRL
28701	59069	A	28876	206	403	
28702	59070	B	28877	1	2046	
28703	59071	A	28878	1	1335	
28704	59072	A	28879	1	974	MEAPPIEDVSSRDNLNRRRNYGH PADLFWFYSLRALPEVYASSD AHEKFVKDFVAAWSLNLVLYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLF VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAISYTMPFWVVFIAALFLG ERLRRGQYFALIAAFGLFLVLQ PWQLDFSSMKSAMLAISGVS WGASAIYAKRLYARHPRVDLL SLTS\WQMHVCRQLASQLPLSH GAMPRCRRPGHSSNPDRLANVI ARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDNLNTQ LWISTNAFRFGN
28706	59074	A	28881	568	717	
28707	59075	A	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	A	28884	1	575	MSGSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTPDWDPSPRWDDGIS GHIADYSITAQTQHAKLNTEDD/ SNESTGSVWQGLWRLQDD
28710	59078	A	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRAILPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHIRIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

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28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVG TG*VE*EEKY NMQT*/E/LENWKPISNLHDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSKGRKNQRSTRTHCHHPS PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDI MLLIALMLQLTCWLAGVHAQK QGWDKHFQANTVRNRNVLST VRLGMEVLRHSGYTITREDSLV AATLLTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWNGTASSDNFPNIFILPQND MALAAAVAPPELEALLAAGKV SVKIQEPCDEILFSRAKVWNGE KWACVTIVGGHTNIVHIETHDG VVFTQQACVAEGEQESPLTVLS RTTLAEILKFVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSSIV IRTSAASDARMGGATLPAMSNS GSGNQGIGTELNVSCRFPATNL FVHDPTQQAMQRNQRRFAVQT FPVWRVAQHCAVRPFRQRIGQ LRDIFHLKGDQFTNRPKIVAF
28693	59061	A	28868	2095	2722	
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPQDPHGILQGAGKEDSQ AQKTTARQKRKTRKTATRQKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQGCVQLFTQ SFTATPAASATTATRPILCSSR ARAGYPSTTGVSRRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPAF/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRADRDHPRIAVVALID KRIRFGISRRFRAQSIIHRIFAQR MHIFRPVIGQHATGNSRLSAS TQRLHHNPAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVSPLIIRADNP FRDEVGFLCQPAVTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGQPAGGAVAVTPGLARAA DADEFVVPVPGVIAVRQQAVQ VLAL*LPGRGISGGEFITA EVRS VSRCSRVRVYSTRGIL
28698	59066	A	28873	2	712	
28699	59067	A	28874	337	383	

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28679	59047	A	28854	383	1367	RPTCWTSIEWVRRVRTAALRSS GKTWVFCCRRRIJAGELMLTNR HTGGVMVTTFRASEAFAGALE LTGKATLVALINRCIGAVIRYM LIAVIPDIFQRLQVVLNVWILAV ANETTVRQRRVRRFKVDLVVR VHLLLHIEVETVGVVTFIGHAR HHAKLSSIETAEIAIAQVFTRRA VETETITRFFFLIHCLTQTFNN GDTFRAKLLVVVNMLAAEQRV NGFVDADVTQRNRRTTVFEDF RNIIVSIETHATSTRYG*CVGPP AMRACSGAVQPVQWLHPGKL RQGEPSRDLVRQRPAALCLPRR HRILRGYNGNIQRRLYSTGNGL
28680	59048	A	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	A	28857	1	1020	
28683	59051	A	28858	1	613	SAGDGARIEQFDRKGMVNNKF NYFIMSKLAEAGIPTQMERLLAS DTECLVKKLDMPVECVVRNR AAGSLVKRLGIEEGNELNPPLF DLFLKNDAMHDPMVNE\SYCE TFGWVSKENLARMKELTYKAN DVLKKLFDDAGLILVDFKLEFG PVQGEVVLGDEF/SPDGSRLLWA QETLEKMDKDGFRQSL\GGLIG AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	1	422	
28686	59054	A	28861	625	750	RNVQALQGAHGTGGALTDPA* QHLGTLCADLL*NGLSPSPRD
28687	59055	A	28862	1	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRGSPGIR RLEHRFEKVQKPGFEVFIPGF KQGKLGRLPGVKALVFGIDTGL FQLQAVKNLDGF*FDEASASQP GSDNILRELVRATGRADGSGT GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	



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28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	
28666	59034	A	28841	162	1760	
28667	59035	B	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAC- ETRMYPEEPVYLPPRYRGSIVIH SIAF
28671	59039	A	28846	855	1134	PGNVLRLLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFACR ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCACVACNLCAVAWP VGCISLVS
28672	59040	A	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ\VTWRLLAAGV CLLTVSS\VARADSLDEQRSRY AQI/KQAWDNRQMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRLLRLHAQYQNTKRVHT QFSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	A	28849	1	1247	
28675	59043	A	28850	533	1029	SKSIMLLCRSVVSMIRRSTVAA FTLAAISVARSVLNLIIIRDIGM QAMPLCRSTTGRNRWTSSAKR TILR*RQRILPLTPC*HRMFRSFL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749	1050	SPHMPGITAGTPFSVPLAISAPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAITLYGSADSPECA RTT/INIGTFLAHFRHVFAHGFG NIIHRHFPG
28677	59045	A	28852	260	717	RQLRTELSAGIAAFRTGNAPAIL RFMKLAPPP*WRRKPLTGV*RV *RGRDSVR*VAFVPTVSAIQQL DPRSLLQQDAFKKAGLDPEQPP KT/WQDLA/VLCRETESLRHEV RLRQRLAGLDPTGKL*AWNMG MPYDADAKDAPQKPLSAEPAC
28678	59046	A	28853	776	2730	

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28648	59016	A	28823	1	1030	MMCIMYRTASSLANQYHIDSE QARRGSQNAFDVNFEAWQLEI NHVLEAASAQSQRNYQISALVF ISMIIVAAIYISSALWWTRKMIV QPLAIIGSHFDSIAAGNLARPIA VYGRNEITAIFASLKTMMQALR GTVSDVRKGSQEMHIGIAEIVA GNNDLSSRTEQQAASLAQTAA SMEQLTATVGQNADNARQALG TGKNAATTAQAAAVQFIDRCQ ADFTRGAYRYSRGTYFICQYLT VTVSGIDAHQRGQTDQTQRILLQ LFLVQFDTHRQTLNDFDPVTGR ILRWKQLDRAAGDITGHRDND TSTLQRQPGVTYFGGSLLHGW *SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLALWLKKHRFRLDQVQN FYPSPLANSTTMYYTGNPLAK IGYKSEDVFVPKGDQRRRLHK ALLRYHDPANWPLIRQALEAM GKKHLIGSRRDCLVPAPTIEEM REARRQNRNTRPALTKHTPMA TQRQTPATAKKASSTQSRPVNA GAKKRPKAAELQCPLVMTSGN LSGKPPAISNEQALADLQGIAD GFLIHNRDIVQRMDDSVVRESG EMLRRSRGFLPTGRGLRIDYKQ KMRGTRRAGCNFNQSGQGRPS LKRGEQTDIKKAKKQATGLAG ESMLQDDAFYAVITHAAGPQG ALPLTPQMLMESPS\ATCSA*RR TPGWAGTPTSSPAKRC*LSALRI TSSGSTPSCSRRHWRKRARRSD ACHHSRFSPTVWPVTQPKKGR
28652	59020	A	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A	28829	1	2649	
28655	59023	A	28830	59	511	
28656	59024	A	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHAYVSGKSRISPHTREA M\NDHSKRAWLYALRRRAGR TRHRCPGRTGRQRL
28658	59026	A	28833	1	727	
28659	59027	A	28834	1	3069	
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRRA FSPDQHPAGNYRTRLSARPFV* RCLYYSR*ARRGNYRQH*TTSP ALYQAASPFQ*SIAG*RAGKTR YRSSVYLCDVHFDHSGSW

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28631	58999	A	28806	167	327	KNNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	A	28807	1	1197	
28633	59001	A	28808	1	4104	
28634	59002	A	28809	1	1368	
28635	59003	A	28810	82	1143	
28636	59004	A	28811	72	212	
28637	59005	A	28812	1	1078	MKDVTLVRPQDAGANTCAHIL SQLPHLQLPTLETGLINALGY APGDMQPSDSATWGVAELQHE GGDTFMGHQEILGTRPLPPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAIGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVIDITQVINIQCRC QQAACGRRKDQCRNQSKENQY GNITQTDITRTIAHGVVIAAMI DNPPRIRKPTKSAS*LWWPLFY LLAVSLFTLWNRVRFHGLSAS SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVDHNG YSGNACTRLHHAGGIRQ**PNF GYSPPASSCGQVSQNSS
28639	59007	B	28814	1	2703	
28640	59008	A	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAPCCASRNG*KSSFQR TLHVSRRHSRTS*SPQVDTSDN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI NAAS
28641	59009	B	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	B	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	A	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRDALPTTE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCGASGFR

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28620	58988	A	28795	379	1703	LKTVLVDGVVKA EKLVEGAKA VLRQAINGDL DWKAKRQPKLE PLKLSKIEATMSFTIAKGMVAQ TAGKHYPAPITAVKTIEAAARF GREEALNLENKSFVPLAHTNEA RALVGIFLNDQYVKGKAKKLT KDVETPKQAAVLGAGIMGGGI AYQSAWKGVVVMKDINDKSL TLGMTEAAKLLNKQLERKID GLKLAGVISTIHPTLDYAGFDR VDIVVEAVVENPKVKKYPSAG VFHQLYCRDVVPMFAIYTFGP QIVGLLGLGVGKNAALGNVVIS LFFMLGCI PMLWLNTAGRRPL LIGSFAMMTLALALLGLIPDMG IWLVVMAFAVYAFFSGGPGNG FNRVKEEFDHERFLVALTNYGT AMCAFEDAARYAN/LARAVWR GYWSFPVDSGKIRPHGDQIKLH EKHAV*SSVESRQRHHHLWRC SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPLKRCFQCSTTHSCI PPPLAATRWPVRRRWRPSMCC WSRTYR\PG*AKRRYTSPA
28622	58990	B	28797	1	1521	
28623	58991	A	28798	348	599	RHFQRSLSRSSDSNP*LDPTLFA SALASRQRVTESWSEHPDPLQ VRRKTEDVKTPPFLQQSAHRS VNIVLWIRGFSPTLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA SGG*TGETAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDHK RPREALLDSLKKLQLDYIDL MHWPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQQ GKG VFDQKVIRDLADKYGKTP AQIVIRWHLDSGLVVIPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	A	28805	300	567	SAGFKKSGTRHCDVRPGACGT TLYQRR*VH*\WSTVHKPETSS SKMHGQRGSGLLAKSLVANVI CSLIRNPLPIMPPLCAFVSLKM IKKRPRRH

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28613	58981	A	28788	1	1795	MWII SCVMKRTAMNCVLWRK RRRKVCASIFTGKNRANQKR NVELFDARCRPLNDAADTVRY LPVLT VQLLDKQPRLT V LKKIL FGLEPYEISTLFEQRQAMLQSIK EGVVA VDDRGEVTLINDAAQE LLNYRKSQDDEKLSTLSHSWSQ VVDVSEVLRDGT PRRDEEITIK\ DRLLLITTV PVR SNGVII GAISTF RDKTEVRKLMQRLDGLVNYA DALRERSHEFMNKLHVILGLLH LKS YKQLEDYILKTANNYQEEI GSL LGKIKSPV IAGFLISKINRA TDLGHTLILNSESQLPDSGTAA CGQSLNVLYQRIVGERKLHTGS LMSAAGKSNPLAISGLVVLTLI WSYSWIFMKQVTSYIGAFDFTA LRCIFGALVLFIVLLL RGRGMRP TPFKYTLAIAL LQTCGMVGLAQ WALVSGGAGK VAILSYTMPFW VVIFAALFLGERLRRGQYFAILI AAFGICTATQRNRLLPCKNQPC KANQYQGTGDVLNQLHIDFRA FSGVMVAGSRQIFANEISSGAS NVGVVIFSTQDSANTFNVLNAS GGSRSVYPVMSDDMNGSSWKF STRMQKIDPALS VTSGQLMSHV
28614	58982	A	28789	190	2058	
28615	58983	A	28790	199	293	RYPPAETELS*RLCRLLR*STTV RL*LCRPL
28616	58984	A	28791	685	1557	
28617	58985	A	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR TATTQRHCRRMHMMTIGYQFQ PGALVR*SRANHFPGRGDVNLS SRYSNAPGRRHQHQMRRGFVA RSQ
28619	58987	A	28794	409	1305	

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28606	58974	A	28781	971	2314	PTNQKKSRTRWIHSRILPEVQG GAGTIPSETIPINRKRRLPL*LIL* GQHHPDTKA WQRHNKKEEL*T NSPDEH*CKNPQ*NTGKPNPEH IKKLIHHDQVGFIPGMQGWFI HKSINVIQHINRTKDKNHMISI DAEKAFDKIQPFMLKTLNKL GIDGTYLKIRAIYDKPTASILN GQKLEAFPLKTGTRQGCSLSLF LFNVVLEVLARAVRQEKEIEGI QLGKDEVKLSLFADNMIVYVE NPIISAQNLLKLISNFSK VSGYKI NVQKSQAFLYTNNRQTKSQIM SELPFTIASRKIKYLGQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMFTFFTELEKTTL KFIWNQKRARIKTI LSQKNKT GGIMLPDFKLYYKPTVTKTKW YWYQNRDIDQWNRIEPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHP* GSIPSRSLLVATTPTRGVTAAL
28608	58976	A	28783	1	1938	
28609	58977	A	28784	1389	1499	
28610	58978	A	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP VHHLWQVLKKILF/GLEPYEIST LFEQRQAM/LQSIKEGVVA VDD RGEVTLINDAAQELLNYHNFIR SRSLPVFVLASACGSGTRRRRA
28612	58980	A	28787	1	419	VRPGHLLDIDDTDMPSLRYS DP EAQRIGQPFKGDDILKALNGEE NVAINRGFLAQALRVFTPIYDE NHNKQIGVVAIGLELSRVTTQQIN DSRWSIIWSVLFGLVGLIGTCI LVKVLLG/IIFG*TYKSQLFEQR QAMGRL

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28601	58969	A	28776	474	1338	PANQKKPRTRWIHSRILPEVRR GAGTIPSETIPNNRKGGNPP*LIL *GQHHPDTKTWQRHNKK*KFQ ANIPDEH*CENPQ*NNGKPNPE HSKKLIHHNQVGFISGMQGW NICKSINIIHHINRTNDKNHMIISI DAEKAFDKIQHPFMLKALNKL GIDGTHLKIIRAFDKPTANIILN GQKLEAFLLKTDTRQGCPPLSPL LFNVVLEVLARAIRQEKEITGIQ IGKEEAPQKQQLFCRYHYHGK RAPQLLIITHLEEDDEWDIIRYY NVMSEEEIKRMKEIVKPKII
28602	58970	A	28777	2289	3225	LTNQNKSRTRWIHSRILPEVQR GAGTVSSETIPNNRKRWTPP*LI L*GQHHPDTKTWHRHNKKRKF QANIPDERQCKNPQ*NTSKPNP AAHQKAY**PSQLHPWDARL VQHMQTNKHNP SHKQNHDKN HMIISRDAEKSFNKIQPFMLKT LNKLGISGTYLKIVKMTMSSS HLFYALCLLTFTSSATAGPETL CGAELVDALQFVCGDRGFYFM EQCTMAVSIRGRELLGPSEQEM LHKESGKQRQKANTIPVTSKIV HLALYATLLLFVMEQFLGESHK SREIFSFEQQISELGKESMKFSEE KEKE
28603	58971	A	28778	1177	1272	
28604	58972	A	28779	480	766	SSEIQHWFQGPWRSCRVSGR RHEASTVLPLCFLLPQNSSSMQ LG*NRSMP/HVSESSRTLVL*EV TKHQVSSNFKMRDKDRSGRAS SLRKHRRE
28605	58973	A	28780	1	1344	

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28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TTNRPRKVKIRHPVASFFHLFFR VSAIIVCLLCELLSSSFITCMSKK WLAVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK LKRARLADDLNEKIAQRP GPM ELVEKNILPVDSSVKEAIIHGKTL KIYYLGAPAEAATKEDERTTSG PGHHATNYHFLLKDFYLSWL HFVHKDAILSGHPLVRL LSTRV LRGPNDVFHGVSSVDSVLAIFV LAEPMGSL SASLEN
28590	58958	A	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPTITGLVRLVV AGANGDRLGQPV TGADVRLSR CRKVMPSRSVEMGLVPSSSVIV TVLPLIGFVLLAFSRGRWSENV SAIVGVGSVGLAALVTAFIGVD FFANGEQTYSQLWTWMSVGD FNIGFNLVLDGLSLTMLS SVTG VGFLIHMYASWYMRGEEGYSR FFAYTNLFIASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY TDPKNGAAAMKAFVVTRVGD VFLAFALFILYNELGT LNFREM VELAPAHFADGNMMLMWATL MLLGGA VGKSAQLPLQTLAD AMAGPTPVSA LIHAATMVTAG VYLIARTHGLFLMTPEVLHLVG IVGAVTLLLAGFAAL*Q*K*HP RHPKHRNAG**TRVLQRGAGC AGAIRVTDHFRG
28593	58961	A	28768	3	2191	
28594	58962	B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSERQFVIISV LLHLLRSALLPTMWSILE*VWC GAEKNVYSVDLG
28598	58966	A	28773	2714	3599	LGSQWH* IYKLPWAVWSFSQY
28599	58967	A	28774	45	188	GKVQCHRGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGRL LKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDAWCVP GTT RKSAWK*GKISGSL SFLPVRDG



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28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHRIIVAKPEQ FWKLRQVMFMAIVISLPTIGER FSPFLKSPILIRPSRCGTTDFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLNATTS **LPFSSGRDSSSRKRRTQAITCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLGTGSPPL ALCRTLCITYPI*CPDRAKALR RPRECVRHD
28582	58950	A	28757	1	850	MPVMFLASLSGKHQGHFPGK ERGKFKIKERGTVATEDRRSGD STFYAIQPTRRQKRYYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFFANGEQTYSQLW TWMSVGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTPSQPR YISSRLSASTRTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHPRPQRLAV CLLAVSEEINADKGGYQRRQA HRAY
28583	58951	A	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGRVCSLRTAFQRSSS EAFTSDLQAAELQNRASNRPAR IGHAHLVIFPVQSSWM*RKLAS PRNNLVIPQEKALKEYIKIGNLV MSLAAAPLNR*GLL/IEWNDND GGCKGACDRVPHQNVTAALNR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLLKEHQDKFTTSLVYLSHDGE SLGENGIYHGLPYAIAPDSQK QVPMLLWLSQDYQKRYQVDQ NCLQKQAQTQKDCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGRTRHPGSRRTLSLPLR HSSDRCNRTSADRSTGPRL/A QPRYISSRLSASTRTTMPVTES MVSDRPSSTRLKPMKSPTDIH VHSGWLYVCSPVAKKSTPMKA GTTAGRPTEPTTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	

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28554	58922	A	28729	2	419	RPRPRPRHMLQGTHRQRHLHA GPGVARRRWGGMARRAARGR PRLRLCIFSRSRQLGLRLRFLSST VNEGDQVKTVARSGHFCGGLS SFSFSSSFSSGKKRPSNSPGSMR LGSPPSGAGRAGGIVTVAC*AR LSTCNTKQ
28555	58923	A	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPT NATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	A	28733	1	1281	
28559	58927	A	28734	114	266	
28560	58928	A	28735	1487	1570	
28561	58929	A	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMATTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	A	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	A	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLWCGAICPLSA KPPAGRAPNAPAASP NRPM T PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	A	28746	134	954	
28572	58940	A	28747	1036	1383	
28573	58941	A	28748	2	589	
28574	58942	A	28749	1	801	
28575	58943	B	28750	14	499	
28576	58944	A	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	A	28753	1	1675	
28579	58947	A	28754	1	522	

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28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPPEQAEQ YQQMIAQLADWLVLKLTGYDA VCMQPNSSGAQGEYAGLLAIRH YHESRNEGHRDCLIPASAHGT NPASAHMAGMQVVVVACDKN GNIDLTDLRAKAEQAGDNLSCI MVTYPSTHGVYEETIREVCEVV HQFGGQVYLDGANMNAQRRD MAGKPGPLTVRKMRGSRVTVR AL*/ASVWIGFDDHRRNLGHTT ASGAIKDQISGYEGGAKSAQPA WDAYMKAVLEGVPEQPLTPPP GIVTVNIDRSTGQLANGGNSRE EYFIEVNEIVVNPATLDWQLA LRQAAGKTDLARDMLQMLLDF LPEVRNKVEEQLVGENPEGLV DLIHKHLHGSCGYSGVPRMKNL CQLIEQQLRSGTKEEDLEPELLE LLEMDNVAREASKILGGHDN GGNALLHKALPPGNVGVKAM APIPPFPQPGKSVTICWKPASS ENRSNLEIFLRELISNASDAAD KLRFRALSNPDLYEGDGELRVR VDEVLSPASVPYS
28551	58919	A	28726	1	1279	
28552	58920	A	28727	3	762	
28553	58921	A	28728	1	1472	MTQDELKKA VGWAALQYVQP GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVF DLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKD FSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GRFGNEYS GWFDLQLKQRVYN ENGKRVD AVVMMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWKVGPGKIDIALVR EDVDDYDRSLQNKQQINTNTID LRYKDIPLWDKATLMPRIPTQR YGLAKA/SLEAD/VRY/MANAM GPEGVRVNAISAGQTRTLAAPG IK\DSRK\MLAHCEPVTPIRRTVT IEDVGNSA AFLCS DLSAGISGEV VHVDGGF SIAAMNERDPFTDL HRYRMNLNMMNYGAQRNM

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28526	58894	A	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLTLLRCVS
28527	58895	A	28702	1	608	
28528	58896	A	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184	
28531	58899	A	28706	478	627	
28532	58900	A	28707	33	1072	
28533	58901	A	28708	35	516	RVVEFADEGQGAALSLWSGS SPETLKLHWPVHVN*IRFSSWK TFRIJRSRDFWADRLMRTLRLNF LSKWDHL*GQTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRRDGGLAGLRGN SGAQGGDA
28534	58902	A	28709	1	777	
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWTIVA*SPR* PRCRCWGS*RGTRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRRQRPPRWTIVA*SP R*PRCRCWGS*RGTRGALPV VRKQPGDPKTPLASCEPNQPV PEAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSLRLLGR PSHEGPWLKGTSCRS GTTCRDR PWV
28539	58907	A	28714	2	1580	
28540	58908	A	28715	286	352	
28541	58909	A	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	A	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLQLVEVLPE ANRQLRQSGAGDGGQAVF*F HRFLASVHQHKAASASPPYLFR IKCPVPRLRAPALLLIDNRLYG
28544	58912	A	28719	1	3534	
28545	58913	A	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTCLKPRKSSKPTF CGCDSLFSPICHFP/HGLSDVALI VQQLRQRG*PLQPARLPVHWR HQNAVVDGVLSGENGAGWG RAWLRIRS
28547	58915	A	28722	225	3465	
28548	58916	A	28723	937	1770	
28549	58917	A	28724	142	484	

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28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI AHPGEELAKKIGVPDAGAIGIM TLTPGETAMIAGDLALKAADV HIGFLDRFSGALVIYGSNYTL ARKTQAVEFNDKGDIDTPGEYF NHPRWYHALITTLQDQDMLSP LIWGFRNYKDVQVIKATPHKIV ILMGILLSPSVFATDINVEFTAT VKATTCNITLTGNNVTNDGNN NYTLRIPKMGLDKIANKTTESQ ADFKLVAMGAASVGLIPL* PEMHQHAHLSLLYRSLVIHLRR QVISVWVSKNGLMMPLSLNL TVRKRYAGAQTRCSPIRVLK
28521	58889	A	28696	605	2021	
28522	58890	A	28697	2256	2336	CIKCCARRIAREPGYLFS**RCK YPG
28523	58891	A	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN V*SWIKSS/MQMGQKMGVKISD EQLDQAIANIAKQNNMTLDQM RSRLAYDGLNYNTYRNQIRKE MIISEVRNNEVRRRITILPQEVES LAQQVGNQNDASTELNLSHILI PLPENPTSDQVNEAESQARAIV DQARNGADFGKLAIAHSADQQ ALNGGQMGWGRIHASLPGIFA QALSTAKKGDIVGPISSGGRFD GTVEVKDGHVINGKIRVTAE RDPANLKWDEVGVDVVAEAT GLFLTDETARKHITADTPAALR WLEENQLEDGHECLLRVSSD GRSRGFINGTAVPLSQLRETSTT TGARRVIRAIRRINSSDASTIPTL MAITISNNTVSDMHSSMTMMS TRIRTLITTIYNGDLRMIRQRKL CKTAIARTYGNDDTFHPGMRH QRMHRVFKNAPHLDPVVTLN IYPKADESSLKASRGTRGAAY RPARQONLYSASSGKKDENPVIE FKNVSKHFGPTQVLHNIDLNIA QGEVVVIIGPSGSGKSTLLRCIN KLEEITSGDLIVDGLKVNDPKV DERLIRQEAGMVFFQFYLFPHL TALENVMFGPLRVRGANKEEA EKLARELLAKVGLAERAHHYP SELGGQQQRVAIARTLAVKH KMMLFDETTDFDPELVHEVL KVIHEFAEKGITNDSLTPAKT QGEGGCLQSQERGPQREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	

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28507	58875	A	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQKWVSSNQKY WLVYKTTDPPRLRPIFSGYQPM CPFNGRPFWIHKNPMGVHWAV ATGLALIPVIGIAEFGWFWFGG ETYMAAWNVSGLTGFGAIQST FNVTLWSFIGVESASVAAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMG MIPNAALRVASPF GDAARMALGDTAGÄIVSFCÄA AGCLGSLGGWTLLAGQTAKAA ADDGL\FPPIFARVVKAGTPVA GLIIVGILMTIFQLSSISP NATKE FGLVSSVSVIFTLVPYLYTCAAL LLLGHHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWWENRLFRKNPARAQKMVL PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAADVMEKQ QISPAQVVVRHNRCPAIVVHLI GRARELSKDLVVG IKNQPATV KAFIRPRTAPDVRLAKLLLQAV NRHFGNVMQMVA A
28512	58880	A	28687	1	709	
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPRVHAHLQPRAAPL*A GEVWK PRLVGRSHWASRPSA LQKGEPGSPSWENACVPQAPH RLLHQQKAF
28514	58882	A	28689	3	227	NSQDFPACGGLCHAELDR TAA GLVHQH\RH PGHTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	A	28691	1	1701	
28517	58885	A	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLPSGA GKSDWSSGDSEKAKTAAHTIY RDAGRVRGYRQL
28519	58887	A	28694	1	370	

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28492	58860	A	28667	1	340	
28493	58861	A	28668	516	734	WTGDWRRTCDRENQHVSGAA RTAFIPTNGAISPGINYSFGH*Y* DCHLPQA*P*LCRAAGQNRCH VARTCLG
28494	58862	A	28669	1	1163	MHTHARETCLALGKPADDATL TAAIEAVGLENAARVLKLYPFE MSGGMLQRMMIAMAVLCESPF IIADEPTTDLVDVAQARILDLE SIMQKQAPGMLLVTHDMDKW GRHADVESQYRYQTTPKIFAG GDAVRGADLVVTAMAEGRHA AQGIIDWLGLDVKLGALEERR KVLQVKTENLQAERNRSRKSIG QAKARGEDIEPLRLEVNLGEE LDAAKAELDALQAEIRDIALTIP NLPADDEVPGKDENDNVEVSR WGTPREFDFEVRDHVTLGEMH SGLDFAAAVKLTGSRFVVMKG QIARMHRALSQFMLDLHTEQH GYSENYVPYLVNQDTLYGVGL YPLGALASGW/WALASGWLPK RRERKD/GDTGAHGVPRGSRKP RIARKVRGT
28495	58863	B	28670	1	4770	
28496	58864	A	28671	1069	1398	VIGAQPVLRIIRKQARRQINRL TLILLHYCLTTKLKNGVKPGIV AAFYFLPGAG*IHPAGCHGTQL *SFGKMRVQYTRVTLSSQASG KISAYLIDLGLKPLKLIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	A	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	A	28677	1	2175	
28503	58871	A	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLD VLMILDAVRELE*TITPAGRRM HCKGACMKPLLDVLMILDAVR ELEKQAIKLHEGWENELVIGVD DTFPFSLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG NLTLDFDTVSLNLQRQTLHS DATVGQPKVESARDAPHIAITP VNALLDDAELAALIAEHDVL D/WYG*RCGT*STERQQR*RG* RSAPAMTAHDRDAIASSSETCA RSRWSVEYASPVCAAPPDSRSKR RSASNSAASHVF
28506	58874	B	28681	1	2298	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLSPKCLK L*SYKSFFKWSPRCSP
28474	58842	B	28649	107	264	
28475	58843	A	28650	301	470	EIQLVLSLSGGGYSHAVLMIVS SHKI**FYKGLFPTFALHFSLLLP CEEGCICFPF
28476	58844	A	28651	2	263	WEKKDTEWRKKVILSSV*LRL VIF*PFSMLMLFHPVWR*ARSH ESHLAITHLWALYF*PPCQICFL *DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMEQC**GGAN IYARRQGADAAGDQGSSCRL
28478	58846	A	28653	1	554	MPTYCPGASLLILTYKTPKELLS IYVSTIRKSRERRNRRLGAR NFRSEEQIYDQWRLDQVGKFFP FPPRENYHFGSEHVGSFSLDK CCNEKLYEVIDLHLKKKFLNTE TSLVKCEVSRCWVTNLNLLPY H/VLFQI*LSWRERQNQSKTTN GSSNGAPDAVHN*NLLWSLGP AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWPALPEN GYMKQFCVSGLGVLFHGCVFL CWHHCCFVL*VWSLGSPRSRG LHLVKAFFLCYPRSNCFLLNWG IVGVVQLRFPQEGCLWCH
28480	58848	B	28655	1	400	
28481	58849	B	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTLALPVSSQPFSLHTA EVQGCAVGILTQGPGPCPVAFL SKQLDLTVLGSPSCLHAVASAA LILLEALKITNYAQLTYSSHNF QNLFSFSLTHILSAPRLLQLYS LFVESPTITILPGPDFNLASHIILD TTPDPDDCMSLIYLTFTPFPHISF FSVPHVDHIWFTDGSSTRPDRH SPAKAGYAIESSTSHIATALPPS TTSQQAELIALTRAFTLAKGLH VNIYTDSKYAFHILHHHAVIWA ERGFLT/IARVLHH*CLFNKNSS QGCFTSKGWSHTLQGPPKGV RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488	58856	A	28663	159	1504	
28489	58857	A	28664	275	552	
28490	58858	A	28665	178	619	
28491	58859	A	28666	3	369	



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28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCS WQKAWAVVCCTFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAAQAAARSSDTRP*PEPH FS\ESVFPRWIFSAFQSLNNFFQA RF
28457	58825	A	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	A	28633	1	1104	
28460	58828	A	28634	194	863	YLLFVKNMSSLEISSCFSLETK LPLSPPLVEDSAFEP SRKDMDE VEEKSKDVINF TAEKLSVDEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISL\EYEA YLPMAENE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFVSS\AHRA AISLKLLSYC/AFDTFKRPRVPI WKK\EIYEESSTWKG NKECFW ASNTLITYVFRACNLNFVKLLL
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCASQCPDTRVHVFLHW WCSSLC PAPVCLSLCRGL*GHF PPDSEDQSSPNC SGYTLEEK LRSQTIPSCNGKFPCPPRAYDG
28462	58830	A	28636	405	800	
28463	58831	A	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	A	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	B	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHIMRCPHISKIS SLYYFNCFRY*DCYCHTFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLN TGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSDEPLFPSP NSSARGRAISST*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGS AVDL SHGLHLGLHL KNDL*FYSFNSGIDKPEIAKLSG CSFGGTFLIWG
28472	58840	C	28647	199	309	

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28431	58799	A	28605	1	1824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	
28435	58803	A	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
28438	58806	A	28612	114	469	VSRPTYAKVFTTSKTAPQKVFP TAWCSA/TGHETALSATQVPIQ WIATAPNSPAPPSDPRRQSWVS QIPSSATSPNFTM*EPRTQEVTE PHDSRPAIPSPAVPRRESCTGRP HLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	A	28615	950	1094	
28442	58810	A	28616	146	822	LGFLRLSEMPRKQGVYRTRIW KFEDGLSNVLVI/PIEQINHMRD VFGSGSERATCLARGRGYINSL ARCQNLVNRDLHDLSLPQDSTL VHYIDDIVLHGFSEEEKGQVAQ SADLDEGLLKIPGDTFGPEADK DFLHKDLSTEIVGQSYNTHHM AQDSIPWNPSGQEPQVREHEAC HHLGSGSPPSWELCEQGPPVTE SFQVLVTSGLDKENMAYMHCG IICSNKKG
28443	58811	A	28617	1	1791	
28444	58812	A	28618	244	416	
28445	58813	A	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLK DQIHVVDKSMRKNQCKNV EKSQNSNSSPHDHNSSPASARA ENWTEYESDKLTEVGRGWVI NSSELKEHVLTHCKEAQNLHN
28447	58815	C	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	A	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKIPFSVLEIRTWHLGR HLSAHCTSCAWPQVACLPLAT HPSTCTFCSLQAPGRPGQSPLS PRRACGPEDLPPPPYV*DLAPSL GPSLGPLMSQSQPRRTPLRG
28451	58819	A	28625	96	295	PWKPHPAWRQRWELCHPPFP/I RPLTAALREQPGLLRSTTVFT LMAREPPQAAADSCLCIVQME A

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28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLHA*PDNLRC CPRSGTAAGSIHQDARLRYSVW RWGLLDRLAAVICRQSTHSRCR RKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	A	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCTRA*PSIPPPAA RRSPKKCSP*KLRLP*LSGKSSS YNL
28423	58791	A	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	A	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGFLPRKRSSRHGKVKSF KDDPSKPVHLTAFLGYKAGMT HIVREVDPRPGSKVNKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDE/CRLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMISHRKFSAPRHGSLG FLPRKRSSRHGKVKSFKDDP SKPVHLTAFLGYKAGMTHIVRE VDRIPGIHRCNKKERWWRAVT HCIRPPPMVVGHLVGIVYVETP RGLRTFKTVFAEHISDECKRRF YKNWHKA\KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKKIYQ VIRVIAHTQMRLPLRQKKA HLMEIQVNGGTVAIEKL\DW REKLE\QQVVPVNVQVFGQDEM DVIGGDQRAKGFKVTRSWPT N*LPFKAHVLGILSRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIK NASTDYDLSKINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	A	28603	1	2133	
28430	58798	A	28604	3	245	

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28403	58771	A	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTQSLFGGLLTQTRMKF GAVTRIG\DLWPWEINPLSSCSLL HEKDPPTTSGPQTHQPKEHLTN FKSGCSSPCRAKSQFFLSLCSST
28405	58773	A	28579	98	617	KALLLTQSLFGGLFTRTRMKFG AVTQIG\DLWPWEINPLSSCSLLR EKDPPTTSGPQTHQPKEHLTNF KSARFKKIKACYHSPATAWPFK AYKLSLQFPHTCPKTRQALQV SSGSVPYQPNCFAYPPHGAKPI YSPILNTSLHNPLFCSGSQTCFL YYSFAPFIPASLRFHLD
28406	58774	A	28580	1	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH FEYVAGGAS/NTLAHVA/QDSEI PGAFGVLTLKA*TNDERAGTKL HGGWGGKCLTACRSALWADL QIRPYDHKNRGSNVHNRVPAS GAAAMAIHCLECGWAPLAAGD NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHIQVSLEINHSYLPGGVIS SLKKMAGRNSERKTVLVKSSF QEVNRGTEALALWENGDFEAP VLTFTTALLPEGATQAFGKENT QKASKERYGSLNITRNNMLQIL NKQQTEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNIDSWKNA GRVFKDSKDFDANDPILKDQTQ EWGSAFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGGVNADVGDVVVRLPVW HRRGGEAVFMQVSRLQILRHLP HGVVAVDRDHHAHRRRRHVA GDRSGSVRL
28410	58778	A	28584	845	966	
28411	58779	A	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKA VDTQ RH
28412	58780	A	28586	464	847	

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28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKH YGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTRDPHYVEDKGH KYL/VFEANTGTEHPQPQIERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHL PDL CSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYM TNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTV
28395	58763	A	28569	2	1778	
28396	58764	A	28570	1099	2224	DGQQLIALHRLALRELQQAVH AGLPQQA KILFDGGSE/TRQNPL QQLVHMGLPRPLDKKNFQEP
28397	58765	B	28571	1	1938	
28398	58766	A	28572	1	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVG VHVLLIVDSCSKL EQHSTLSRAILLIYKGFCFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNH PGAQYANRLSPRVGRFINAAGTTG FPTGKRAVSATQLMDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLV KRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQGGEDSPNRFDDGG RKKQIRTVRQFIDEGNNTPADT QTLRDPHYVEDKGHKY
28400	58768	A	28574	6803	8521	
28401	58769	B	28575	2010	17745	
28402	58770	A	28576	1	1060	

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28392	58760	A	28566	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFFKR GAIFRVHKHAVNPMSPKCRRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKET/YPKQQQNEKYQVPQF- DQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGR VFKDSKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGINSNDI YMLGYVSNSLTGPYKPLNTTG LVLQMGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

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28387	58755	A	28561	3	2077	
28388	58756	A	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETYGVS HITRHDMLQIPKQQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVG NSIDSWKNAGR VFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNEGI LPISEPIKQDFRLLG
28389	58757	A	28563	610	2303	SLPNLDNAAICSSSSSPTRTR*SL SEGATQAFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDN SIDSWKNAGR VFKDS DKFDANDPILKDQTQEWGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTRLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSLGTLQGFPAPAWLALAH VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGPKAKAKATAGWRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNQSEHQTY ESIVIDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEVDVRIILT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPVCNEIFDRLIKPRWEIR
28390	58758	A	28564	1	2079	
28391	58759	A	28565	1	774	

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28378	58746	A	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAF KENNQKAYKETYGVSITRHD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNIDS WKNAGRVFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHGKQSLTTAQVNV SKSDDTLKGVEDHKTIFDGD GKTYQNVQQFIDEQNYTGDP EAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKP DGS GIVSLKIDWIIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIKAWIIERY QPPQSYQRMPDFRRRFLQSRPA CMHDWLCAEALAWSIQTASYL VTMQVNLTSLSDDTDRLSVVS NSGWVSSGSLVRFNTIKTSSGEI KRTVPRILPDPDDPRSAIEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLLPKAVHLA
28379	58747	A	28553	2372	3570	EALLPGDQDSQSGKGVAAREV WFLPSSFAPVLLRLVGNHHVG DNSIDSWKNAGR/VFKDSDKFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHGKQSLTT AQVNVSKSDDTLKGVEDHK TIFDGDGKTYQNVQQFIDEQNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQA KKRDAELANGALGIIELNDYT LKKVMKPLITSNTVTDEI
28380	58748	B	28554	1	2232	
28381	58749	B	28555	200	2602	
28382	58750	B	28556	1	3198	
28383	58751	A	28557	1	2169	
28384	58752	A	28558	1	2259	
28385	58753	A	28559	1	2418	
28386	58754	B	28560	1	1974	



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28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNSC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFTQFRLSETK EITNPYAMRLYESLCQYRKPDG SGIVSLKIDWHIERYQLPQSYQR TSPCCCHMKKDVFASTMISS SRVSNNTSKTTIHKNCQKDDSD RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGGVR RCLQQQCEQTVRILHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTTDDTSGTVVQSDYQTDDTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	B	28551	1	1954	

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28355	58723	A	28528	793	1382	NTTAAGR VIRLTSENGSHTTFR YDVLDR LIQETGFDGRTQRYH HDLTGKLRSEDEGLVTHWHY DEADRLTHRTVKGETAERWQY DERGWLTDISHISEGHRVAVHY RYDEKGRLTGERQTVHHPQTE ALLWQHETRHA YNAQGLANR CIPDSLPAVEWLTYGSGYLAG MKLGDTPLV**ERPADR*ASDG ASPADGSTALAA*DQTCVQRA GAGEPLYTGQPARRGMADERQ RLPGRHETRRHTAGGVHPRPPA PGNAAQLRPL
28356	58724	A	28529	1039	1689	
28357	58725	A	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	
28361	58729	A	28534	3	273	GKLIAVIGDEDTVTFLLGGIG ELNKNRHPNFLVVEKDTTINEIE DTFRQFLNRDDIGAFRLGLCW LRNRKPDHLPPLPCA VTQCH
28362	58730	A	28535	2	415	
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRQSWVSRLR*CQEAAG MADSCPRSGGAILAFKSAPEVI RRALSAQSLRATSSSSASGAGA FCLSPSKYFPETSASSSATARYV LGWAASSGLLTSSQKMG
28367	58735	A	28540	1	400	
28368	58736	A	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTCHLQRVVFKNISPAD AHRNLCLALRGHKT VTYLTLQ GNDQDDMFALCEVLRHPECN LRYLGLVSCSATTQWADLSL ALEVNQSLTCVNLSDNELLG*G C*VA VHN/S*DTPSAFLQRVV GKTGHLTEANLQGTLLLCWVF SRELTHLCLAKNPVNTGVKYL CEGLRYPECKLQTLVLWNCIT
28370	58738	A	28543	1	2633	
28371	58739	A	28545	127	2030	
28372	58740	A	28546	1	3066	
28373	58741	A	28547	259	3222	
28374	58742	B	28548	1	2640	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28335	58703	A	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC WIMFIDLRMLNQPCTPGMKPT* SWWISFLMCCWIRFASILLRIFA SMFIRDIGLKFSFFVVS LPGFGIR MMLTS
28336	58704	A	28509	765	950	LLPQFQNLLLVYSEIQLLPGLVL GGCMCPGIYPFLD FLVYLHRG VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SQKEWYQLLFVPLVEFGCESIW SWAFFGWQAINYCLNFR TCHW SIQRNF FLV*SWEGVCVQEFIH FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI* TLK
28339	58707	A	28512	1	1641	
28340	58708	A	28513	1	2307	
28341	58709	A	28514	1	3793	
28342	58710	A	28515	178	674	ERPRIMDLA GL LKSQFLCHLVF CYVFIASGLINTIQLFTLLWP I NKQLFRKINCR LSYCISSQLVM LLEWWSGTECTIFTDPRAY\SS MGKENAIVVLN HKFGN/IDFLC GWSLSERFGL LGVSQKCIPPCL THFFGSAPPLV FLLLVIQNLQKN QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI* TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	B	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	
28351	58719	A	28524	1	1089	
28352	58720	A	28525	91	507	AGTASASPAPNRSLSGSEPTSSS VTQENGADVQGH ERPWKAR SRRFCPMEGTFRKVPSHGSHVP EVSMLWKACSGSFRPVEGHSV RCALTPASGCSP*AGTASASPAP NRSLSGSEPTSSSVTQENGADV QGH ERPWKARSRRFCPMEGT FRKVPSHGSHVPEVSMLWKAC SGSFRPVEGHSVRCALTPASGC SPSKSKATVGCRCSD FCTVEEF LQKIFLQVESLDRRPRCLPLT
28353	58721	A	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFTAE*RP GTDNR ADNRQ

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28332	58700	A	28505	1	1699	MDEFLDTYTLPRLNQEEIESLN RPITSSIEAVINSLPTKKCPGPD GFTAIFYQRYKEELVPILLKLIQ TIEKEGLLPNSFYEATNILIPKPG RDTTKKENFRPISLMNINAKILN EILATESSIKKLIHHDQDSFIPGM QGWFNICKSINVIIHHINRINNKN HMIISVNAEKAFDKIRHLFMLK TLIKLGIDETSLKTVRAIYDKPT ANIILNGQKLEAFPLKTGIRQGC LLSSLLFNIVLEVLAIRAEKEI KDIQIGREEVKLSLFADDMIVY FKNPIVSAQNLLKLIGNFSKVSG YKINVQKLQAFLYTNNRQTESQ IVSELPFTIAAKRIKYLGIQLTRD VKYLFKENYKPLHKEIIEDTNK WKNIPCSWIGRINIMKMAILPK VIYRFNASPIKLLNFFTELEKN CLNFIWNQKRAHIAKTILSKKN KAGGITLPDFKLYYKSTVTKTT WYWYQNRIDQWNRTEASEIT PHIYNHLIFDESDKNNQWGKDS LHNKWWENWLAICRKLKLD SFLTHYTKINSRWIKDLNAGSKI QYHADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRSSCHRQSAPS LSRVGRSSQIRSALSAASGLWR RKPASAKFGRPRTGSLHLPVK* KAFVSLQESSA*MNLRQ*PE*D WISWIN*QNFGN/CQGSTLKIPV VERKILDLYALSKEHSFSPATEQ SWTENDFDELREEGRRSDFSE LKEEVRTHRKEAKNLVKRLDK WLNRTSVEKSLNDLMELKTM AREQLRDECTSFSSQFDHLEER KYKLPSSENKHLIYANKLENLEE MDKFLETYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKNSPGPD RFTAKFYQMYKEELVPFFLKLF QSIEQEGILPNSFYEASIIIPKPG RDPTKKENFRPISLMNIDAKIFN KILANQIQHHIKKLIHHDQMGI PGMQDWFNIRKSINVIQHINRT KDKNHTIISIDA EKAFDKIQQCF MLKTLNKLIDGTYYVKIIRAIY DKPTANIILDGQKLEAFPLKTST IQGCPLSPLLFNIVLEVLAIRAVR QEKEIKGIQSGKEEVKLSLFAD DMTVYLENPIISAQNLLKLKSN FSKVSGYKINVQKSQAFLYTNN
28334	58702	A	28507	1	1428	

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28322	58690	A	28494	173	527	
28323	58691	A	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSPALPCSLKYPFYD HRTKFTLTTPFSHTLAQKENQ SPLKHMGGKRLQNIFLPIRP*DQ TPWLLERS
28325	58693	A	28498	921	1008	
28326	58694	B	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLDLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFSASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVSPLPGFGIK MMLAS
28330	58698	A	28503	1	957	
28331	58699	A	28504	41	412	IALIILRYIPSIPSLLRVFSMKGC* ILSEASASIEIIMWFLSLVLF*W ITFIDLHVLNKPICIPGMKPS*SW WISFLMCCWIWFASILLRIFASM FIRDIGLKFSFFVVSPLPGFGIRM MLAS

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28304	58672	A	28476	1	1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGGFANCLSL YFGYLQIKARNELGVYLCNLTV ADLFYICSLPFWLQYVLQHDN WSHGDLSQVCGILLYENIYIS VGFLCCISVDRYLAVAHPPRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMHHEEVIEDENQHRVCF EHYPIQAWQRAINYYRFLVGFL FPICLLLASYQGILRAVRRSHGT QKSRKDDIQREVLSTVIVFLACF LPYHVLLLVRRYWEASCDFAK GVFNAYHFSLLTSFNCAVDPV LYCFVSETTHRDARLRGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQMQS\KLKIYSRPLDR PASPCSDVNDIEGTPPEISTAQ
28305	58673	A	28477	1	717	
28306	58674	A	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	A	28484	1	34	
28313	58681	A	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	A	28487	505	716	REPCPVSQREVWRPGCLD/HCP RQSGSLGETLRGTAEQPWPHS QVLSNLRVLQLPLISLPSLRRRA LFPA
28316	58684	A	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPTYKGCE GPLQGELQTTAEGNKRGYKQM EEHSMLMGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHTT*LQ/YTTTRL Q*PK*HGTGKTEI*INGTEQSP QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	

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28297	58665	A	28469	1	1901	MPESPTPLLGRDILAKAGAIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDFAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQQECHQATQV LLNVLATCGYKVSQKAQLCS QQVKYLGVKLSKGTRALNNEE QIEHNCQQVIAQTYATRDLLE VPLTDPNLSLYTDGSSFVEKGL QKGGYAVVSDNGILERNPLTPG TSAQLVELIALPRAELGEGKR GSSSICFLSFLVPPMTIYTEQDL YNHVVPKPRNKRVPILTFVVG GGLGGLGTGIGGITTSTQFYK LSQELNGDMEWVADSLVTLQD QLNSLVAVVLQNRRLDLLTA KRGGTCLFLGEECCYYVNQSGI VTEKVKEIRDQIQRAEELQNT GPWGLVSQWMPWILPFLGPLA AIILLFLFGPCIFNLLVKFVSSKI EAVKLQIILQMEPQMMSMT/KI YHGPLDQPASPCSDVNDIKGTP PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD LLEVPLTDPNLSLYTDGSSFVE KGLQKGGYAVVSDNGILERNP LTPGTSAQLVELIALPRAELGE GKRGSSSICFLSFLVPPMTIYT EQDLYNHVVPKPRNKRVPILTF VVGAGGLGGLGTGIGGITTSTQ FYYKLSQELNGDMEWVADSLV TLQDQLNSLVAVVLQNRRLD LLTAKRGGTCLFLGEECCYYV NQSGIVTEKVKEIRDQIQRAEE LQNTGPWGLVSQWMPWILPFL GPLAAIILLFLFGPCIFNLLVKFV SSKIEAVKLQIILQMEPQMMSM TKIYRGSLDQPASPCSDVNDIEG TPPEEISNAQPLCPN*AGSSWS SRRPTSPTALGFSC
28303	58671	B	28475	1	1989	

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28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQIHAIPIKLPMFTFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPTYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKLLK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWE LNNEITWTQ EGEYHTLGTTVVGWEGGGIAL GDIPNAR
28295	58663	A	28467	1	1863	
28296	58664	A	28468	2	1308	



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28275	58643	A	28447	142	772	LVNVDVDADLVGLCVSHRHTV EEQYSTLALLNHGPQVALKYV HMDEVMPACCLEGGQCLPAL CGECKLQGSFILSAPGRQGSQR VGPREAQGHIVIGRKLSTALM LIGGQRLEESAAIESGCMEATP QGMAGSPQVGQAQSPVNPKE PIGDF*GGSQDYRGGIQKPID*Q CGPVL/SRQSELWCGGRSHSVE FLLGSAASAPPGPGQA
28276	58644	A	28448	1	1935	
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSLYSSEFNNS FVDALGSD\QDSGNEDVFDME YTEAEAEELKRNAEVIVFIPEYS WSNSVSLFPLCPGAKGPTFSVH CRVHFGPFSSH
28279	58647	A	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	A	28459	3	161	
28288	58656	A	28460	992	1102	
28289	58657	A	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV GFPQGCQLVHIW*M/PLDAGPE HNSLKGFLVPLFPLAATPRAPG TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMRLRLQKRLASSVLRC GKKKVWVRPL*TNEIANANSR QQIRKLIKDGL\NRTPTAHSWP SCRTNTLSRRMGHS*SLRLLD PVNM*GLLNASWITKC*LLDPV NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVWLDPNETNEI\ ANANS\RQIQPEASSKMGLIIRK P\VTV\HSRA\RCPVKTPLARRG RGRATWGIR*GGKGYKPNARN AQRKFTWMRENGGL*TRGCL RKIPVNPCKDRIANMY\HSLLE G*RGNVFKNKADFSWEHIHKL EGRQRPRKKAPWLTQA*GPAG S*DPRKPRKRR*RAPPRPKKEEI HQRLFSKE\EETKK
28293	58661	A	28465	221	350	GPSSFRLPTLSSLHVSHGREET* HSLET*RDAVSLRIFKSLSV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK YVGLWDFKSRTDEELSFRA GD VFHVARKEEQWWATLLDEA GGAVAQGYVPHNYLAERETVE SEPRDTQAVRHYKIWR RAGGR LHLNEAVSFLSLPELVNYHRAQ SLSHGLR
28256	58624	A	28427	3	438	
28257	58625	A	28428	37	403	
28258	58626	B	28429	1	1176	
28259	58627	A	28430	2	2150	
28260	58628	A	28431	1593	3025	
28261	58629	A	28432	322	2168	
28262	58630	A	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	C	28435	52	363	
28265	58633	A	28436	1	3363	
28266	58634	A	28437	1	918	
28267	58635	A	28438	1	1422	
28268	58636	A	28439	3	10899	
28269	58637	A	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	A	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTDILLS/HS GGRGAEAPTMC LKLT VSKRAC FEGLE\WQFNLWRNKK**C*DK KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQLAALAPRVLTGG LADVTALLRAPATPGRLVAGA RGGWGYVQSCRGAGAAAVKP LGSAETAVPIARLGCRRFSRSRC CRRRGRGSLLSFSAAKPIVFKEK LTMKTDLSLMEEKLECSLWCCL SDPSTPGRCCVLERRIVPWMQQ LLANIKQAEKHEKNHPEVTVA MALTDIDLQLQFSMSQPE/GPPS PGSRPS*PPPAALLWTPAGQA CPGPGGAEEADPSRNSTEWLRP PHHSSDCLRGLAHIVSQWVSEC LLCSPGSPPRSPLWALCWEHWE TWPALPEGNQPSPEGLPPCSRS QWPQTTPASDPQ
28274	58642	A	28446	3	213	LTQHCWTHLVRSSHRTGSSRL HNHQLHQPCA*S*LCQKEHASR GWSEQFNLWRNKK**C*DKKH KTAG

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28241	58609	A	28412	1	903	MAKKIQLTYKCVQNWVVLGL TDFKNEAADPRRVKLQTFVVS VTALKAARLELFIPPGGFVVS ASGVKLQTFVSVTAHKGSD PKTRHKGSPSPHQTPESWLHP VDPAPGLQVELPASPAPCARTP QPLGGQWDWVPWSRGRCSG RLGPRSSPRWGAGSGMAGCRS RALPHGEAAKAQRKVTAAGP GAKHLTAWGQQQLATPSVG PAEPTHTQNSHWPASAVCSPSS RLRLSLHTYPQAEAGAGSLGQP RKGLPQCSSLKGSAAKVGA QAEVPRASEACEG*RAPQVLP KWEPRQRRCRERARPARAAS LSPLISI
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL YHPQ**WNQQQLHHRCLLQG SIHLVFGPQWDPRRRRPLRGTR SAMARMDILRISREYITQEITEA ATKRKVLSPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPCRALALL SPWVVDGTGRRGAGGGARQG GWGSTGAHGVGRRLRHGLQ VPSPAPRESS*GPARNRSQRRRS DSSLRERK
28244	58612	A	28415	27	363	
28245	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQRS*SLSGPHQTY DISSYTCQCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRVALLSPWVVDGTGG CGAGGGAHRGGWGCTGAHGG GGRLRHGGLQVASPAPREGS*G PARN*AQSRWAGTAGGPSTPSA AAGPGAKPLIAPGRQGNPCH WCGARQAHAPQLATSAW TRAFRECVSPA WPSCLGAACFH CLLIGPFPFSFSSQHLSTSLGHLV LLSWHLTSLSVSFRILTRLLRVF TGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	A	28425	1	599	

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28228	58596	B	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	A	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	A	28403	204	4198	
28233	58601	A	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMFTFITQLLLVVEV KDSLRLAVEVVFILQKAMYE KQAHYMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*DTLLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	A	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTQEPSWLHPVDP APGLQVELPASHAPCARTPOPL GGRWDWAPWSRGWCSLGRLG PHRSPWSGWEAQA*QWIPHQG CRWSCLPVTRRLVALLSPWV DGTGRRGAGGGARWGGSGRT GAHGVGGRLRHSRLQVPSAL LFKYYYCDIFK
28239	58607	A	28410	1	609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTFA VSVTALKAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCFDRA LIGAFTIPELDTKVLHVPIRLVR YRVWTQRFSKAPPDSGAQLASP SESHTRAAGGAACQSQCRA LLSPWVVDGTGRRGAGGGGAHR GGSGCTGTHGVGGRLRHSLQ VPSSA*VSHPLRGFL/LQPEPPR* APPPAPRRPVSTTQGLRSAGA RHWDWQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRRAALRAVTLTAK VCSFTPVGLYWLSQPMVAVLRE PESNLIGWSQWPFRLLKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCGSPGATLIQWRMAS MD

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28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDGTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLFLRILPL FADKVPKTAENFRALSTGEKG FGL*GVPCFHRHPIPGFMCQGGDF TRHNGTGGKSIYGEKFEDENF LKHTGAPGVLSMAKCWDPTQN GSQFFNLALAKTEWLGWASHV GVLAK*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRILWLSLAVPFWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMEQRGNNCEPKVGKQ VTLQHSDPEDRKTSTRCGENLY MSSDPTSWSSAIQSWYDEILDF VYGVGPKSPNIVLLVII*IIERIPR TNKEHLVPV
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSIVQDCMDKGCII* LRHTSGNCMYVSDKFDFKEQCI FSPRSSQKSLSGNDLQK
28216	58584	A	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHFLTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEEFFH ILEYYDKTLSSKISYNDFLRAFL Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	A	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDPEMENKGGQTL NNSSLMAEAPGTMCRFTLAPH VLAVQGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	A	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPLPARWPDSL MQLARQVSRLESGQ
28223	58591	A	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	B	28396	518	1606	
28226	58594	A	28397	1	798	
28227	58595	A	28398	737	3067	

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28203	58571	A	28374	2	1455	SAAVAARSPQPQRPSATLGPGP QRRPPSAAPTPAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP VTIAEGPSPITSEGASEANLG\DL QKKLEEELE\LDEQ\QKKRLEAFL TQKA/RRVGELKDDDFERISEL GAGNG\GVVTKSPAQDPISGLIM VARKLIH\LEIQAGASGNQIIPR/D LQVLHDGTWPTMGG\FYGA FY SDGE\ISICIEHMDGGSL\DQVLK E\AKRIPEEILGKVSHRSFSGGL AYLREKHQIMH\RDVKPS\NILV VNSRGEIKLCDFGVSGQLIDSM ANSFVG\TRCYM\APERLQG\TH YSVQSD\WSMGLSLVELAVGR V\PIPPRDAEELEAIFGRPVVDG EEGEPHSISPRPRPPGRPVSGHG MDSRPAMAIFELLDYIVNEPPAP KLPNGVFTPDFQEFVNKCLIKN PAERADLKMLTNHTFIKRSEG\ EEVDFAGWLCKTPAG*TKPGTP VTRTAV
28204	58572	A	28375	229	257	VSLASPLVSLAGRSPSRPLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPTP
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQK*PGGTEDS/YDASGPPPKF LIKEIKLGVPRFFPIRGV*NP GPG KNFGGPFFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESSPI LLRWMTTSTTKSAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378	1	1001	MSWEMEQDEVYKEMSINHKN EGTRVEKPNRYRIIHQPDAINH VSRKKDVPSASGAGHSRSSTGS RPGVRRLLWPLLLRSAPSGPLNN AVPAPGKGPGRWGGSPSLSRSG GKASTRVAPGLSAHSQAASGV PEPAEPQHQRTKASGSRRSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRRRRWACRGLR GRPGA VSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDVHMPKHLELADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSSAPGDCACHPT PQPSRDWQASV

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28193	58561	A	28364	620	1246	GSTWHGWDGSRCSQRWWS MTKRSSQPSSLS*SRSSRRWMS SSPNW*KTGPSSMSRMSSAG* SAASSRSCATRWTRRRPAAWR G*GVTPVAWWPPWTCSWSRPR EPGSGWPKPSVCWNSSEMRTT MSSSGSSTPWPPVSRRRPWTER RLGSVRGDRLRERSRPAVNRT RMSRVPSGAPRGTPSRWWMM MKCWDHQMRLVEEEVG
28194	58562	A	28365	86	402	KGWWCRRKKGWNWKRWFLET FLQGLLEGPHPPSPTAPRRTT* SLYSAPSRMVQVLLDDLHKWF LYSCLVSAISIGIKFPLKIHISPGS GVLEARETMSHFKEAAL
28195	58563	A	28366	54	353	
28196	58564	A	28367	66	352	
28197	58565	A	28368	442	700	HWNKVPAENPHLPWVRCSPPT PLGKPKPCSSWNRRSGTDVSGT GLSESGSSWPSGSCNGVTGTDA YGPVGYVKSGSFPGPRVRGT
28198	58566	A	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR SKDATPDPPRGLGKFPRLPQA PRLGSRLLSTLCSTLSGRGG KNTSRLSFSPSGSVKGRVRDVK EPGPIRAHRTAFFPNASSGSEG R*SPSVVAWRGFR/CVGVWRFP TVGVWHAPPRCTR*SPITGSAP LSVWSPACTGSPTCTAGA
28199	58567	B	28370	163	387	
28200	58568	B	28371	112	419	
28201	58569	A	28372	1	1902	MSRIAWKLLWKLIQGYLGQPA GTARRHPGIGIFKSPPGDFTCNG LIAVIKNQSDNQRMSPGWSWSP GRENNPTLVEVLEGVVRLPETV HTAVRYTSIELVGEMSEVVDRN POFLDPVLGYLMKGLCEKPLAS AAAKAIHNICSVCRDHMAQHF NGLLEIARSLDSFLLSPEAAVGL LKGTALVLARLPLDKITECLSEL CSVQVMALKKVFGATSRVA KLFREGLKAHGNSFETSGEAER CCTWRPKEMTCVE
28202	58570	A	28373	1	2019	

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28181	58549	A	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVVISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLSLFSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFPVCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	A	28355	2357	3083	FFSLFFFHILASGLSILLIPSKNQL LDSLIF*RVFCVVISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNASQIFWYVVSLSLFSLVSKNIF ISAFISLCTQ*SFRSRLFSFHVVE RF*VRF/CNPEF*FDCTVV/WRD SLL*FLFFYIC*GELYFQVCGQF WNRCGVVLKKMYILLIWSGEF CRCLLGLLGAELSSIPGYPC*FF VLLICMLTVGC
28185	58553	A	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVVISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNVSQRFWYVVSLSLFSLVSKNI FISAFISLCTQ*TFRSRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR DSLL*FVFFYIC*GELYFQLCGQ FWNRCGVVLKKMYILLIWGGE FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	A	28358	1	1263	
28188	58556	A	28359	77	304	
28189	58557	A	28360	1	756	
28190	58558	A	28361	1	369	QQRTLLASNEAFKSQAKSASQP ASKYMKENDQLKKGAADVGG KLDVGNAEVKLEENRSLKAD LQKLKDELASTKQKLEKAENQ VLAMRKQ/SPEGLTKEYDRLL EHAKLQAAVDGPMCKEE
28191	58559	A	28362	879	1156	
28192	58560	A	28363	54	407	



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28171	58539	A	28341	2	367	MTMHYEIPVTRRRSGT*LPQ NA/SVNNMPH*TGAI*ADISMTN YARIERNHLGRGNSNSKDPKLR ESSEHLRKLKTRVVNEQTRLGL IMETFVGRGGEAPFYFQCDKHL SRSFQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLAF*SHRSW LSSPWPSDLWRPWAGGACARL LLQQPRDSASLKERQQPQSGAY R*NSHLPGTEHLGEGVAVCAAS ADLNVACWL
28173	58541	A	28344	1	269	
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQLCGQFW NRCGVVLKKMYILLIWGGGFC RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSISDLSCFPLWAFSAINFPLHT ALSASQRFWYVVSLSLVSKNI FISAFISLCTQ*SFRSRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR *FVIISVLLHLLRRALLPTMWSI LE*VWCGAEKNVYSVDLGWR VL*MSIRSAWCRAEFNSWVSL TFCLVDLSFSLAALNIFSISTLV NLTIMCLGVALLEEYLCGVLCI
28179	58547	B	28350	1	3135	
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNC DVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQVCGQFW NRCGVVLKKMYILLIWGGGFC RCLLGLLGAELSSIPGYPC

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28154	58522	A	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG SLFWTSRMPSSVFPCTLTSPFSL PLRIP/PDHTSQLTWTVLPPGFR DSPPLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSEASCQQA TLDLLNFLANQGYKVSRKAQ LCLQQVKYLGLILAKGTRALIK ERIQPILAYPCPKTLKQLRGFLG ITGFCQLWIPGYSEIARPLYTLIK DTQRANTHLVEWESEAETAFK TLKQALVQAPGSLPTGQNFSL YVTERAGIALGVLTQTRGTTTPQ PVAHLSKETDVVAKGWPHCLR VVAAVA VLVSEAIKIIQGKDLIV WTTHEVNGILGEKEYGYQTN AYLDTRRSALRDWCFKYARPV AAILLLLAFGPCIFNLPVKFVSS RJEAIKLQMLVQMDPQISSTNN FYRGPLD
28155	58523	A	28325	830	1143	
28156	58524	A	28326	234	510	PWQSLP*VAQKVPKDHRSLPLE P*TRSLNNS*QHWLCPPARAP STCSTSCPARDGPPPPSPAPHGP RNTSVPG\HSRPGSPPP\PPRTPP VS
28157	58525	A	28327	2	816	
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRRMFPAQEEADRTVFVGN LEARVREEILYELFLQFLIAGPL TKVTICKDREGKPKSFGFVCFK HPESVSYAIALNLGIRLYGRPIN VQYRFGSSRSSEPANQSFESCV KINSHNYRNEEMVVGRRSFFPM QYFPINNTSLPQEYFLFQKMQR HVYNPVLQLPPYYEMTAPLPNS ASVSSSLNHVPDLEAGPSS

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28148	58516	A	28318	1	2502	
28149	58517	A	28319	1097	1417	
28150	58518	A	28320	1	398	MTAEERDKFPTDQQAIPSMDPH WDPDSHDGWSHKHLLTCVLE GLRRIRKKPMNYSMMSTITQG KEENPSAFLKWLREALRKYTPL SPNSLRGQLILKDTFITQSAADI RRKLQKQALGPEQNLEALLNQ ATSVFYNRDQEEQAQKEKRLSS RSVTIRGILGQSVTRPEAHKGL QDIVKHLKAQGLVRKCSSDCN TPILGVQKLNQWRLVQDLGLI NKAHPLYPVVPNPYTLLSQISEE AEWFTVLDLKDFAFFCIPLHSDS QFLFACEDPTDHTSQTQTILPH GFRDSPYLFGQALAQDLGHFSS SGTLALQYVDDLPLATSLEASC QQATLDLLNFLANQGYKASRS KAQLCLQQRDGQTTLYSNQGA PEGKYSSSRMRPRVRNSLQNLK AGPSTTPALSLPTGQNLSTLYVT ETAGIALGVLTQAAGMNPQPV AYLSKKIDVVAKGWPHCLRVV VAVAILVSEAIKIIQGKDLTVWT THDVNGILGAKGSLWLSDNCL LRYQALLLEGPVLPQIPMCAALN PATFLPEDGEPIS**PLTLRWPLP QLPLNSEASLLLLHQFSYLGMP LVGGSSHEPA
28151	58519	A	28321	318	363	
28152	58520	A	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP PLPARWPIH
28153	58521	A	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD TSEHLKEQTADTSSLRTVTLTA RVCGFILEVSETKNSPEGTNSG HILTSQMGLSPIAKRRETSASAA ALVSATIPICRVQGPLRVLGQE VFLLLLRLPTAPLPINDKPP/PN/ TPLPRRKQAKKSPKDHKNPWAI GYVPFKQ*GEGNLA*PGYMSPS

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28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSFLVQ LLTPCSAQFSVLGSPGILAMV GEDADLPCHLFPTMSAETMELR WVSSSLRQVVNVYADGKEVED RQSAPYRGRTSILRDGITAGKA ALRIHNVITASDSGKYLCYFQDG DFYEKALVELKVAALGSDLHIE VKGYEDGGIHLECRSTGWYPQ PQIKWSDTKGENIPAVEAPVVA DGVGLYAVAASVIMRGSSGGG VSCIIRNSLLGLEKTASISADPF FRSAQPWIAALAGTLPISLLLLA GASYFLWRQKKEKIALSRETER EREMKEMGYAATEQEISLREKL QEELKWRKIQYMARGEKSLAY HEWKMALFKPADVILDPDTAN AILLVSEDQRSVQRAEEPRLP DNPERFEWRYCVLGCENFTSGR HYWEVEVGDRKEWHIGVCSK NVERKKGWVKMTPENGYWTM GLTDGNKYRALTEPRTNLKLPE PPRKVGIFLDYETGEISFYNATD GSHIYTFPHASFSEPLYPVFRILT LEPTALTICPIPKEVRRVPPI/AD LVPDHSLETPLDPGA*LMKVGE PQAGK*HLCFSLPTLGAEGLPF
28137	58505	A	28307	1	2220	
28138	58506	A	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAQRSP AEKMGETPGAASVIRLGGGRV ALRRHVRGEPLRAPDCPLGPDA WVPTRGSHFPGFPPREQSL/W GATPPSYRSSEVRSGAESGRPAP DSVGSQGVQAH
28140	58508	A	28310	1	1066	
28141	58509	A	28311	77	273	
28142	58510	A	28312	1	415	
28143	58511	A	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPRVRRRAMGISRDN WHKRRKTGGIRKPYHKRKYE LGRPAANTKIGPRRIHTVRVRG GNKKYRALRLDVGNFSWGSQ CCTRKTRIIDVVYNASNELVR TKTLVKNCIVLIDSTPYRQWYE SHYALPLGRKKGAKLTPEEEI LNKKRSKKIQKKYDERKKNAK ISSLLEEQQQGKLLACIASRPG QCGRADGYVLEGKELEFYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

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28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLL V QLLTPCSAQFSVLGSPGILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLICYFQ DGDIFYEKALVELKVAALGSNL HVEVKGYEDGGIHLECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAASVIMRGG GEGVSCIIRNSLLGLEKTASISIA DPFFRSAQPWIAALAGTLPILL LLAGASYFLWRQQKEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTPDVILYPDMANAIL LVSEDQRSVQRAEPPHDLDPNP ERFEWRYCVLGCESFMSEHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVILDYETGHISFYNDTGS HIYTFLLHASSEPLYPVFRILTLE PTALTVCPIPK/GREFPRFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIIP

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28130	58498	A	28300	842	2592	IREEVESLKRPIITSSDIEAVINSL SIKKKVQYQTDSPNSTRGENL GNTIQDTGMGKDFITKTPKAM ATKAKIDKWDLIKLKSFACTAKE TIIRVNRQPTWEKIFEIYPSNK GLISRIYKELKQIYKKKTNDPIK KWAKDMNRHFSKEDIYAACK H/DEKMLIITGTWMKLETIILSK LTQEQKTKHRMFSLIPDDGNS LRRMLLIGISVKTPVGTGAIPG PVGGTTAAGAYGRKEKALSNC DSILALALAKMSENQSMESFF EKGKDPMRROQKTLTLTKKKN AFKRKYQESYLNYGFIATVRAS FLVANCIVKAKKPFTIGEELILP AAKDICYELLGEAAVQKVPHV PLPVSTITRPIDEIAEDIAQFLE RINESLWYTIQIDKSTIADNKAT MLVFVQYIFQEDVHEDVFFQES LRATSQPLKTPQTGKEVWHDPF VDKPSESTLSMLEEDQLEIAN DGLKSMFEKTSNLHIVCIKVK AEYPEIATKALRRLAAPPWVAA VDRECQWGSRDVEMRRLDPK AGFSLLGVGNCHCLRTLEFVGL SMSSLCGAMLLCGLRAAPYISL RDHKGQGTLL
28131	58499	A	28301	1	1662	
28132	58500	A	28302	2	406	CWWDCKLVQPLWKS VWRFLR DLELEIPFDPAILLLGIYPKDYKS CCYKDICT/RVCVPAALFTIANT WNQPKCTSMIDWVKMWHIY TMEYYAAIKKDEFMSFAGT*M KLETIILSKLTQEQKTKHRMFSL YWKS
28133	58501	A	28303	1	1404	
28134	58502	A	28304	68	2269	

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28114	58482	A	28284	179	445	QLSGLASGMRESRDVLGLRFTP LLLWIVHSRAWALVESAVMST WECWVGDERGTGVKLAGAHT ELPTGPGV*YSPPCVHVFSLFNS HL
28115	58483	A	28285	128	381	
28116	58484	A	28286	1	1392	
28117	58485	C	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTPAPLPFLGRRWGTWGFP GHAFHSWFWYSTGEGAMGSF LALLSFPLGMKLAILEDFFGIS GTAAPLGSSFGSSLRSSLSVTEA LLARSL/HFLLILLPLLFLLLFLIA FORTLLVGQCPAKSPLGNALEC NLGAAGSRAHGGEHATGGLQL LALFEAGQSLQPLTACVPGPRP LTCL
28119	58487	A	28289	693	905	EESIS*KWPYCPSFHNHLPQAY KAIPHPASLGKT*YNQDNNNAG KLFKANRNPALGCQQPVCST DGFRF
28120	58488	A	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	A	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	1	351	
28126	58494	A	28296	1	507	
28127	58495	A	28297	1	543	
28128	58496	A	28298	343	428	
28129	58497	A	28299	785	1178	

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28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLS
28089	58457	A	28259	1	253	
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	A	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	B	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	B	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGLL*QF WRLEVQYQDAADSMSSGGDPLS HS
28103	58471	B	28273	125	197	
28104	58472	A	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGNKNNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETTGTVTFRHLHCL QQSR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	B	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLCLCQALVSG*CWPHK MS*GGFPLFLTGTIVS/GRNGTS SSLYLW*NSAVNPSGPGLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSSLFA
28110	58478	A	28280	3	610	TDFCFWLPGLSVLFLSFFLSF FLSFFLSFFLSLSFSFSLSLFLS VLSLFLPSFLFLSLSLSLFLS LL/YCLSFLSLSFFLFLSFLSS SLLFSSLLFSSLLFSSLLFLLLLL LSLSLLFFLSFLFSESVLWEGSV AGLQTPALSSALNRAVLVSCS MIDQLCDPGKYFISLCLFLHLR VRTCGVWFVSVLVIVC
28111	58479	A	28281	203	470	QAKSVWKKILSFRI*LHRMSDG IFWLCFYISMHLWCWLVLVWAV WFKLQTTLSRWLTDSLPVSY GYCQGMNEGCSSQFKTVFPTLF SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKG/LTKTPRLLVMSPSSCSR RGIWPNPDTCPLLLL
28113	58481	C	28283	1	603	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28074	58442	A	28244	39	200	LPLFLIECPLFPSPA*LPWPGLPT LC*IGVVREGIPVLCPFSGMLP VFAHSV
28075	58443	A	28245	225	314	
28076	58444	A	28246	243	311	
28077	58445	A	28247	21	1593	RKRTAPAGPRRHPKHCECPNCG SGKGRPS/CSQTHPPPGKLKSSP *SRKAENSKNQSAFSPPKDHSSS PVMEQSWMENDFDELTEVGFR SLAETQQQKEKFRPISLMNID VKILNKILANRIQQHIKKLIHHD QVGFIQGMQGWFNICKSINVIH HINRTNDKNHMIISIDAEKAFD KIQQPFMLKTLKKLGIDGTYLK IIRAIYDKSTASIILNGQKLEAFP LKDRTRQGCPLSPLLFNIALEVL ARAIHQEKDIKCIQLGKEKVRL SLFAEDMIVYLENPIVSAPNLFK LISNFSKVSGYKINVQKSQVFL YINNRRQESQIMNEFPFTIARRR IKYLGILTRDVKDLFKENYKP LLKEIKEDTNKWKNMPCSWIG RINIMKMAILAKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AV VCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPAPPWARVRPPEKC GAPTCSHPREEAPRLASPAGKN VTPWGETQGSGR LGVTGEPE LLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPD\PPAP TPTDAEGLPQQQQLPQLEPQPE CQGPVEAEARQLKSCMKPVRR RPAEEELKTKNMDDNTFAMAE HPDVQESVGPLVAPTPLRPWPQ MTLQVCWSLLEFHSRCLPGY HQURLQNSKDCCFLP
28081	58449	A	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKSS
28083	58451	A	28253	1010	1294	QRFWSQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKS\PE GSAKHGKEQPIPTAKTCQIVK TIQA
28084	58452	A	28254	41	812	
28085	58453	B	28255	1	2957	
28086	58454	B	28256	650	3212	
28087	58455	A	28257	1	556	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28061	58429	A	28231	488	2358	RLSLGHWAAAGKQGASDSCEKP TQPPSGVLESTTP/CAAPSPPNR DSGPCPASSPGLSRPLLSGTAW APPPAPPWARVRPPREVWRAD LLTPQGGGPATGVSGGECDSP VGGNPGIWKA WGHRRTRVAGI GRRGGPGEADKQPLLVLRLQTG SGVDLQQTPTDLQLRVLTVRR NTNKRKGHPHQNPICSTPSSKT EGRSMRQKVNDIQELNSALH QVDLIDIYRTLHPKSTEYTFSSA PHHTYSNIDHIVGSKALLNKCK RTEIVANCLSDHSAIKPELRIKK LTQNCSTTWKLNLLNDYWR SKRKTHSKASRRQEITKIRAEK ELETQNTLQKINESRSWFFENIN KIDRLLERLIKKEREKNQIDAIK NDKGDITTDPTKIQTITREYYKH LYKNKLLNLEEMDKFLDTYTL PRLNQEEIESLNRPIITGYEIEAI NSLPTKKSPGSDGFTAIFYQRY KQELVTFLKLFQSTEKEGILPN SFHEASIILIPKGRDITTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHDQLGFIPGMQGLFSTC KSINVIHHINKTKDKNHMIISID AEMASDKIQPFMLKTLNKLGI DGMYLKIIRAIYDKPTANIILNG
28062	58430	B	28232	1	2664	
28063	58431	A	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPACPKRAPE GSTKHGKEQVPATAKTGQIV
28064	58432	A	28234	804	920	RDIYSNKCPEKPEKI*NGHPNI TIKRIREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	B	28236	3	1555	
28067	58435	A	28237	895	1389	GELLEVMTLAWSWGLFLARII QTQVFKAFLNLFVLIRSSWAF WTHGDELWALVSRKPK*HPGF CDHAPSTFPPPGLCPEPTPPGA VSQYPCPPSPCPWRWLVLPLP VLGTSSPWKGFSPYPPCCFSPF HLPARFLHRGNCLSTFDLVVLP PLEMPVLALS
28068	58436	A	28238	704	799	EKRKSNCLCLQMT*LCI*KTPSS QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	B	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	B	28242	1	1059	
28073	58441	B	28243	1	924	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVKAI IMQLGTLLTFLHELVPALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNWS*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	A	28217	2383	2651	
28048	58416	A	28218	125	1396	
28049	58417	A	28219	466	643	
28050	58418	A	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	A	28222	2	499	
28053	58421	A	28223	192	351	
28054	58422	B	28224	1	2103	
28055	58423	A	28225	247	400	
28056	58424	A	28226	288	589	WCSRRRGWYLLLGFNHYWRSS TFLVRCTPSCPGGCCPRYGIYPV RSCPRLPGGVSRYSIHSG/RWC SWSPSWSPWLTSVTPRLYVAL M*AVVCPVVGKQP
28057	58425	A	28227	319	398	
28058	58426	A	28228	1299	1506	
28059	58427	A	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPLQMT*LYI*KTPSS QPKISLS

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28033	58401	A	28203	3	1626	SEGEAKGSITLTVCTALYLKLT LFHKTGVFGPLRFPVNTLNPS PFHDGTRELGASEAIGQCQSSA AKLRRSGKESESLGPEFQGLWK WLPGSSQCFARESLKLSLCF RPSDPGAEPPTAVRPITERSLL QGDEYCCALGQGVNPWSTDR YWNWATLQEIGPSSCRKTSSGL PLILRYGHVRDLHGSSSHHRPG GPKRNKWFRELGLGSACCMRP RDLVPCVPAAPAVAERGESTA QAVASEGASPKPWQLPGGVGP VGAQKSRIEVWEPLPIFRMYG KACMSRQKFAAGAGFSWYVPV AVVGAKVHDVNLHMLSFPSK WKLHTCMKFGAVTQIVTSLGR SSCSLLEKDPPMVL RPTSPRNI SPISNLTKETRFIRGPKTPAPVT DWEGSLPLVFNHCRDASLIHP GFRGVRPRRDACLSPSPLANLIN LTFKVYNRKKLQFLAFTVRQ TSAMSPAHNKFNQSLNLSGQAF LQNLLPQELATSARNPATRPRN ACSPGFLLSHVPSVRDPTGNWT VQLTWHPLPEPLELWPKAL
28034	58402	A	28204	921	1009	
28035	58403	A	28205	1	1005	
28036	58404	A	28206	1	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPEN\PMKSCK/S QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKY\LKDVHLTRN QCVPIPDYNG*QLGQVCRRPK QMGP GTTKGR\WPQKGVLKFL PAHALKTAEM*C*TLRVLDVDS LVIEHI\QVNKAP\KMRRRTYR AHGRINPYMSSPCHIEMLTEK EQIVPKPEEEVAQKKKIS\QKKL KETPTLWHGE
28042	58410	A	28212	3	466	
28043	58411	A	28213	1	2772	
28044	58412	A	28214	1	1353	
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR S*DY*CWR

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28029	58397	A	28199	1	532	MRVRNREEGNVGKWGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQSESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDYTFCSPGSFSCTH S/SVESHNYHCSRPGLOSGLPHY SRYHT*PS*LHSLIHLTFTPFPHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRPVLPVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFSLSPCCLHCQGRLCG HHEEARRRKNVSIPRKEAGIIHC KGHQK\ASDPIAQDNAYADKL AKKAASVPTSVPHGISQAPPPLP THQARYWQIDFTHMPVRKLLK YLLVWVDFTGTGWVEAFPTGSK KATAVISSLLSDIIPQFSLPTSIS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLLTLFSDSAHLHPG EINNHVAHTRPVWWSLHTDVH EIWCRDSDRGTSLSGRSICPPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGFLFLSSPTSLTVPQPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCIIAGTPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28017	58385	A	28187	221	1634	KNMETEQPEETFPNTE'INGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSPDSSGP ERILSISADIETIGEILKKIIPTEE GLQLPSPTATSQPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RVVECIKIILDLISESPIKGRAQP YDPNFYDETYDYGGFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMPPSRRDYDDMSPRR GPPPPPPGRGG\RGGSRARNLPL PPPPPPRGDDLMA YDRGRPGD RYDGMVGFSADETWD SAIDTW SPSEWQMA YEPQGG\SG\YDYS Y/AQGGGRGSYGD LGGP IITQVT IPKDLAG/SLFIGKGGQR\IKQIR HESGS/SSIKIDEPL\EGSEDRIITI TG\TQDQIQ\NAQYLLQ\NSVKQ
28018	58386	A	28188	218	497	
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28021	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYAEIG NR*GRNLGLTEVTGAVCEALR QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN FSSFPLVENGDAFYLAATLRA PGTVAQGS LTPSQIFSA*WRHPS ISPFS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ SPWNSGPRLS D*LLPRSSGLSG
28026	58394	A	28196	372	782	LRSADLPWEINPLSSC SLLHEKD PPTSSGPQTDQPK EHLTNFKSE KKETRFIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSSKSHFSGG RGKSLQVPEIWPPGQGMPAA QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQQWQHEGWC GQLLPRGHGPNRKLQQQRQWI LL*VPEILPLGQGMPAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL SYPQYLP LLPIYSVLDLRHAFFT IALHPSSQPLFAFT* TDPDTH*A QQITWAALPQGFTDSPHYVQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28008	58376	A	28178	250	687	AATSLPFRASIASANSILRVGV MTSIHHFVFSKRVCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQTQIKSVRPDYLLVE PPHHMGPSFFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	C	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	C	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	A	28183	19	428	
28014	58382	B	28184	61	2118	
28015	58383	A	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSPDSSGP ERILSISADIETIGEILKKIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RFV\ECIKIILDLISESPIKGR\AQ YDPNFYGWKPMDYG\GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGGRPMPPSRDYDDMSPR RGPPPPPPGRGGRSGSRARNLPL PPPPPPRGGDLMA YDRRGRPGD RYDGMVGFSADETWDSAIDTW SPSEWQMAYEPQGGSGYDYSY AGGRGSYGD LGGP IIT TQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSEDRIITITGTQDQI QNAQYLLQNSVKQYSGKFF

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27994	58362	A	28164	1	712	LNSEGNSSGSGDSISYDAPAGNS FLEDCELSRQIGAQLKLLPMND QIRELQTIIRDKTASRGDFMFSA DRLITLVVEEGLNQLPYKECMV TTPTGYKYEKGKFEKNGCGVSI MRSGEAMEQGLRDCCRSIRIGK ILIQSGGETHRAQVYYAQFPPDI YRRKVLLMYPILQTG\NTEFEA VKVL*DHGVHPSVIIQLSPFLIP HGGQ\SIHQRFPEFPI*PTEVHPV APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLLQMPYGCCE QNMVLFAPNIYGLDELNETQQ LTPEIKSKAIGYLNTRYQRQLN YKHYDGSYSTFGERYGRNQGN TWLTAFVLKTFQAARAYIFIDE AHITQALIWLSQRQKDNCGFRS SGSLLNNAIKVNHSGASFDLSI MISARMRIGSDNVKNSKGKPQ RKIKPGWHQKRGDRTKVDCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	A	28171	1	372	FRRVACVGSAGD\TAGAEP/RG ACATAWVCEMAADISESSGAD CKGDPRNSAKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPKQEAGISE GQGTAGEEEEEKKKQKRGKT
28002	58370	A	28172	1	731	LSRGSAAAGGRALGRPWGARRV ACVGSAGD\TAGAEP/RGACAT AWVCEMAADISESSGADCKGD PRNSAKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPKQEAGI SEGQGTAGEEEEEKKKQKRGGR GQIKQKKKTVPQKVTIAKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKFSCGASVTGEDEIIIQ DFTDAIINDVIQEKWPEVG**QPL EDLGRK
28003	58371	A	28173	335	2297	
28004	58372	A	28174	23	416	
28005	58373	A	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	A	28177	1	1587	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27977	58345	A	28147	163	593	GFLEVQTPHPPNLDGPRRANRN TFLWTCHVGIPDLPALPAPASFL GTQLTLKKASDGPRTKEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGVKENGTTGGVVK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQLCIL*S/CWRERKK FHLGKRVELRQGTTLGRVGWP KRRLSQGSAGCFPAGLAHSPPH LAEAPGSGFCTALFEWL
27979	58347	B	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160	1	1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIIIGHVDSGKST TTGHLIYKCGGVDKRTIEKF EAAEMGKCSFKYAWVLDKLL AEREHGITIDISLWKFETSKYY VTIIGAPGHRDFIKNMITGTSQ A\DCAVLIVAAGVGEFESWYSP RNGQTREHALLA\YTLGC*NKL IVGVNKMDS\TEPPYSIQKRYE EIVKEGSTYIKK\IGYNPSTVAF VP\ISGW\NG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPR LWRALALQSYPPTRPTDQAPLR PASPRMSYQKLGGIVNVATEV KSVEMHHEALSEVLPGDN/VGA FNVKNVSVKDVRRGNVAGDSK NDPPMEAAGFTAQVILNHPGQ ISAGYAPVLDCHTAHIACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAAIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQT\VAVGVI K\AVDKK\AAGAGKVTK\SAQK
27991	58359	A	28161	125	370	
27992	58360	A	28162	156	547	
27993	58361	A	28163	108	919	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27951	58319	A	28121	39	346	QYISELQFLASTVRQTPATSPA HKNFQTPEPQQPGIPPEPPPGAC YKCWKSGHQAKECLQPGIPRK/ HASHLWQPLPEPPGTLAQGS LTDSPFDLLGLAAED
27952	58320	A	28122	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKHELTNFKSAA ED
27953	58321	C	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPPLS/CALTL*G DPPTTSGPQTNQLKEHLTNFKS GPHWKMDCPHTPAATPRAPGT LAQGS LTDSPFDLLGSA AED
27955	58323	A	28125	1	354	
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFQLSP**NKITLLKPASS AISALAATPRAPGT LAQGS LTDSPFDLSLAAED
27959	58327	B	28129	1	320	
27960	58328	A	28130	1	605	
27961	58329	A	28131	273	529	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKHELTNFKSG PH*KSDCSTAPG\ATPRAPGT LAQGS LTDSPFDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGSNFHHNEIRSLAAT PRAPGT LAQ/GLTDSFPD LLGLAAED
27963	58331	A	28133	112	331	LGLGDLP\WEINPLSSCSLLHEK DPPTTSGPQTDQPKKRLTNFKS ATPRAPGT LAQGS LTDSPFDLLGLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	B	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28146	1	573	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27934	58302	A	28104	2	1287	GRVGFASATAQSPRILRSEPVRTP PIPAFSPLKTLRIMSLHQFLLEPI TCHAWNDRDRTRPVCLDYISLV VSFEIKK*IALSPNNHEVHIYKK NGSQWVKAHELKEHNGHITGI DWAPKSDRIVTCGADRDAYVW SQKDGWVKPTLVILRINRAATF VKWSPLENKFAVGSGARLISVC YFESENDWWVSKHIKKPIRSTV LSLDWHPNNVLLAAGSCDFKC RVFSAYIKEVDEKKASTPWGSK MPFGQLMSEFGGSGTGGLVWH GVSFSASGSRLLGWGSATDSTV SVCWMPSKSLQVSTLKTFLPL LSVSFVSENSVVAAGHDCCPM LFNYIDRGCLTFVSKLDIPKQSI QRNMSAMERFRNMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRKFCCTTGIDGAMTIWD FKTLESSIQGLRIM
27935	58303	C	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	A	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	A	28110	2	272	
27941	58309	A	28111	39	543	
27942	58310	A	28112	1	789	
27943	58311	A	28113	401	912	
27944	58312	B	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL ALRVNLNVFNKRINSLGKNLAFN LFVYNKANSMP*RLLWKAPRS DK*IQ*SLRIQNQCTQISSTAVH STVTKLRIKSRTQPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL KSGSGKVYQGPAGKAADTTIL SDEDFHGRWGSASLTLRRHSLV AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRKSGHWAEECPQPGIPP KPRPICVGPB*KSDCSTHLAATP RAPGTPAQGSLTDSFPDLLGLA AED
27950	58318	A	28120	32	143	

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27922	58290	A	28092	1	2438	MRLFGYARVSTSQQSLDIQVRA LKDAGVKANRIFTDKASGSSSD RKGLDLLRMKVEEGDVLVKK LDRLGRDTADMIQLIKEFDAQG VSIRFIDDGISTDGEMGKMVVTI LSAVAQAERQRILERTNEGRQE AMAKGVVFAENDKKMLSNAFI ETADFRTLIEDDRITIVVGRGT GSFNLARAATRLWRYAMLME IASYISSHYKLSSQISSETLLNEH LKKWNSAQGDILRKCRVAK YLDENNPEESIGDLQFNLNISEI ENNIVSLLERSDRKVILMDKL DEAYEPDNIGIGMIAGLAYASIE LNQKAKCIRPIIFLRDNIFRSLSK EDPDYSRNI EGQVIRLHWDWA QLLMLSAKRMKVAFKLDIEKD QRVWDRCTADDP*KGGNGFKR CLQFTLYRPRDLLSLLNEAFFSA FRENRETIINTDLEYAAKSISMA RLEDLWKEYQKIFPSIQVITSAF RSIEPELTVYTCLKKIEASFELIE ENGDPKITSEIQLLKASGILQSL YSVGFVVGIRDKNTSSYSFCHDG RTPDKGFESNEKLLIHPCYWLG LNLNRNALAPEEAEINDEYDI NIISDNSAIRNKTIGQITTHLDQI PIGNEGATEFEQWCLDALRIVF ASHLTDIKSHPNGNAVQRRDII GTNGGKSDFWKRVL EYKTRQ VVFDAKNFEELGPSEYRQLQSY LTGPYGLGLFIINRDESEVVRSK
27923	58291	A	28093	673	916	
27924	58292	B	28094	1	4725	
27925	58293	A	28095	959	1387	CMRRPSCSPASIRDNTAPHSRT LKVLIIIGKRSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVCIS RCMSAVMVMAVLTIA CRFLKM TVSVGHICSLNFALQTSTTAMA VPAAATRASRAQPNGRHPWRI CWKTQKA
27926	58294	C	28096	997	1302	
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTG FYAHL LRHYKTPVG HS*Y*WKLHGENKSSAFVC*P TCRNPFIDCW
27933	58301	A	28103	390	1186	

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27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIIGKLSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIIGKRSSGRKLSRILPLLRS SSSM*PTRAPN*SSASFTFTSVSP L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	A	28077	31	117	
27908	58276	A	28078	1	547	
27909	58277	A	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMSTF KVLLCGAVLSRIDAGQEQLGRR ITILRMTWLSTHQSQKSILRMA
27911	58279	A	28081	1	1785	
27912	58280	A	28082	551	685	
27913	58281	A	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPRV ACASAWGAGTDVTGWAAAMP RVGRCLPRTGLGSARLLRPEL GGGAGPAPEAMRFGADAGST EQPRLPARS*PRLPQRPRRPRKS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPRTSPE SS
27915	58283	A	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	A	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY
27919	58287	B	28089	743	852	
27920	58288	A	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRANY

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27894	58262	A	28064	107	2499	PIEDPEGRRRMREFILRSIQGVL RMAPQIQPKPLLTKSSTSVSQA RL/TSKQKALLPRQCSGSAKAQ AEREKIEETCQVGMKPPVPGGY TLQGKWITTFCNQVQLDTIKIN GCLKGKLIYLLGDSTLRQWIYY FPKVVKTLKFFDLHETGIFKKH LLDAERHTQIQWKKHSYPFVT FQLYSLIDHDYIPREIDRLSGDK NTAIVITFGQHFRPFIDIFIRRAI GVQKAIERLFLRSPATKASVSK LKCFWEPTRGTKYEASQVTG AFPLRPKKGAATPSQLVIVNSS DAHNKCDEESEVRIKSTLGLKL DCKKGTAITKGTKEDEEDGAM SGVDQLCLLSSVDSSGRPQLMT DWHGVKGQFSCFKCGEEKELQ QKRKLTGKGWNVFFMVLEVG KTKIKALEVLASGKGTA SWFIQ DFLAVNSSHGRWGKKEEFLFQ KWKVDPWLPVRWELVQTGT THLVPEGRSDSVTCAWMP LGS KQVYKEPAGFPDMLRLRGS RV RMAVVTVHSQRLNLSLGDQHF NYPLPLKKKKKKKKKDTLIYPA DWLESCQSDNLSLAERDLVLV LRLALCALYGLLAPGNNGTESA ELHPGDKTEAQRPMALFKVTR PLNERPGDLASHVSRFAKSFLK PAMESLECPQSRLVGEARKGHS ELVEKIERGCESTVGE GTTRKG SKRDHLDSQCKLGQRSQPWGQ
27895	58263	A	28065	1	1770	
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	
27898	58266	A	28068	1	882	
27899	58267	B	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	A	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV AAERAGAQEAAAGAGPPQLGG LIAWATHLQHSAAVPLLSQRM CHTCCLSPRKL VIGCRAAKSLSS SPCGKWLC AALIRQPSVKGLPS CGVPLPLSLSRIQMCSSEATSSW ELNPDFGEAATSP**ESGF/LQS VVSTALLPDNTTGETFHHDGRA DIGSQFIHRFLVCCHELLVLRWLI TLDTKADVVDIGHRLRCFDCRC VDSTICD
27902	58270	A	28072	1568	1819	

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27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNNFFFFFFFFFFFFFFFFFFFF FLLLPLLLPLLLLLPLLPPLLP SSSFFLLLSSSHSSPSSPSSPS SPSSPSSPSSSSSSSSSSSSSSSS SSSSSSSSSSSFSSFSFSFSFSFSF SFFFFFFFFFLFED
27880	58248	A	28050	544	729	
27881	58249	A	28051	1667	1896	
27882	58250	A	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFFFFF/ ILLVLLLVLLVLLLLLLLLLLLLL LLLL/ASSSSSPSPSPSSSSSSSS FSSSSSSSSSLSLGAYVLYFMVT HSSPVLCCLCNLIINNI*EE*FFR FRHNCDFLAASLTGVDWLL
27884	58252	A	28054	47	376	
27885	58253	A	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	A	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDYKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPPPQS*TPPRE*VPSFSSG VGKSS
27889	58257	A	28059	165	408	
27890	58258	B	28060	21	253	
27891	58259	A	28061	1	150	
27892	58260	A	28062	1081	1303	
27893	58261	A	28063	147	437	

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27870	58238	A	28040	1	594	MLDITNDQGNASQNHNAIPPYS CKNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTP LHPPALLAVDRGSRSSVPATDS LPSAHDRQQQFHTWVCSRLLA TVRADPADGQQPQARADVCGC RGTGFINLVMIHLMGFEVGRIQ QLEQVAPRPQGVSWVDSSDH LQGSPrVEPPGTWDLRVLCSQG Q*EAVNCGPQTPGLD/SFDYGH SCRSKVVSCHGFDLHFPDH**C KNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTPL HPPALLAVDRGSRSSVPATDSL PSAHDRQQQFHTWVCSRLLAT VRADPADGQQPQARADVCGCR GTGFINLVMIHLMGFEVGRIQQ LEQVAPRPQGVSWVDSSDHL QGSPrVEPPGTWDLRVLCSQG
27871	58239	A	28041	1	285	
27872	58240	A	28042	1	1059	HNLSSNSFPKMSFPNSSPAANT FLVDSLISACRSDSFYSSASMY MPPPSADMGTYGMQTCGLLPS LAKREVNHQNMGMNVHPYIPQ VDSWTDPNRSCRIEQPVTQQVP TCSFTTNKEESNCCMYSDKRN KLISAEVPSYQRLVPESCPVENP EVPVPRYFRLSQTYATGKTQEY NNSPEGSSTVMLQLNPRGAACP QLSAAQLQMEKKMNEPVSGQE PTKVSQVESPEAKGGLPEERSC LAEVSVSSPEVQEKESKEEIKSD TPTSNWLTAKSGRKKRCPYTK HQTLELEKEFLFNMYLTRER/R ALEISKSVNLTDARQVKIWFQN RRMKLKKMSRENRIRELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSL/SFFFFFFFFFFFFFFFFFFFF FFFLFFFFFFFFLLLLFVSFSFSFS SFSFSFSFSFSFSFSFFLLPSSSSS SSSFFFFFFFFLLLLPFFFFFFMEH
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048	3	212	



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27843	58211	A	28013	3	353	GYIEKRISCIALLF/SF*IPVNFLR FHDTFI*FCYSS*SIQLSLWQSQI LLCV*LLRSIDFLYLIW*PLTYN EHASILLSLRAPYQLFDL*NDRS HIRYSATLVNPAVCFAVGHD
27844	58212	A	28014	106	1814	
27845	58213	A	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	C	28018	80	328	
27849	58217	B	28019	1	1074	
27850	58218	A	28020	602	853	
27851	58219	A	28021	505	649	
27852	58220	A	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	A	28024	1	219	
27855	58223	A	28025	2	508	
27856	58224	A	28026	1	1011	
27857	58225	A	28027	1	699	
27858	58226	A	28028	175	351	
27859	58227	A	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	A	28033	1	788	
27864	58232	A	28034	115	358	LIVVRSRRGTSRSGSPRATAMA FKDTGKTPVEPEVAIHRIRITLT SRNVKSLEKVCADLIRGAKEKN LKVKGPVRMPTKVK*IVVRSRR GTSRSGSPRATAMAFKDTGKTP VEPEVAIHRIRITLTSRNVKSLE KVCADLIRGAKEKNLKVKGPV RMPTKVK
27865	58233	C	28035	179	283	
27866	58234	A	28036	57	431	
27867	58235	A	28037	54	440	RVPELVWGTEVKERKNARSGV PSTQRLECGSAESAAGAPASVS VQVTAVPAPLFPGWTTGGGRAV NLTEAERM RVVINSVCHWRLY E*TANRFS*KQDVGKLTNCVCH PEGMLKAVTTQAQVFLVIRHN
27868	58236	A	28038	1	2693	
27869	58237	B	28039	131	350	

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27833	58201	A	28003	1913	2388	PIIHNTTAMKKAACAEPFTTIV CTE*AILSQRTCSL*FTVINDICP GPAH/VVQDIHGKLTGSAIA NRFQDAMAIPFLGTQGKRVPR NGMAIPFPGNRNVIAGAFIPHR QHLGQIQLNPVRQCSNLFALL AQRSEAFHMRHRHRTVKK TILF
27834	58202	A	28004	1	1566	
27835	58203	A	28005	951	1217	
27836	58204	A	28006	1294	3108	
27837	58205	A	28007	1	1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLLDI DINDPLAVRDRAMLEV MYGAG LRLSELVGLDIKHLDESGEVW VMGKGSKERRLPGRNAVAVI EHWLDRDLFGSEDDALFLSKL GKRISARNVQKRFAEWGIKQG LNNHVHPHKLHSHFATHMLES SGDLRARGAYLCAKLLSGAAQ VPEWRSFAFWFARCAEQARQN QYLQVSSCPALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISGQNALLDKLDAFR HLTLDGHCPGLGGKELNAYITA GIENCHESYQLEEGRRKLQLGM SLMIREGSAARNLNALAPLINEF NSPQCMLCTDDRNPWEIGHEG HIDALIRRLIEQHNVP LHVAYR VASWSTARHFGLNHLGLLAPG KQADIVLLSDARKVTVQQVLV KGVEPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFIAVLERYGQR LAPACGLLGSGLNELGALAAT VSHDSHNIVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE GAKERMMGKRYKETSIGSLK VPAPLNLNLSLQPREQLGGQST
27838	58206	A	28008	1	3257	
27839	58207	A	28009	1	2145	
27840	58208	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQGGPGGKRFGTAPATPGCL VHDL*APCLRWYQHPTEEELR ILAGKQQKGGKTKKDRKYNHGI ESKPLTIPKDIDLHLET KSVTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTVEYYNFMKPTQEMN ISLV

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27815	58183	A	27985	3	529	DAWAFHKMAPKAKNEAPAPP KA\EA KAKGF*RAKKG SF*KVS HSH\KKKKIPHVHPTFRAGRPL R\LRQP\KYP SGRALPWRNK\L DHLCLSIKFP\LT H*VLPMKKIE DN\NTLVFIVDV KANKHQIKQA VKKL\YDI\DVAKVNT/LWIRPD GEKNGICSDLA PDYDA\LDVA NKIGII
27816	58184	A	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS PHCGGIQAHLFNL*RD LFKIWT
27817	58185	C	27987	175	363	
27818	58186	A	27988	724	958	
27819	58187	A	27989	3	823	
27820	58188	A	27990	1	877	
27821	58189	A	27991	487	786	
27822	58190	A	27992	147	623	RS AVANGLTKRRMGLKLN GR Y ISLILAVQIAYLVQAVRAAGKC DA\VF KGFSG LFCSS LGDTMAQ LPAGPGDDKTNIKT V\CTY WGG ISHSCTVTALTDCQEGAKNMW DKLRKESKNLNIQGSLFELCGN GNGAAGSLLPGFPVLLVSLSAA LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLQKS REYSCSSFISLSSTDAHCVLSE YARPLS/QRPAPNGSSPRCQASE AQSPGHRPPPPLFSSPLAALQLD SHRFPSDPNGKDESRPPRLCTKL GRGCAGCGK
27824	58192	A	27994	1	800	
27825	58193	B	27995	54	165	
27826	58194	A	27996	46	313	
27827	58195	C	27997	30	151	
27828	58196	A	27998	169	1173	
27829	58197	A	27999	456	651	
27830	58198	A	28000	487	833	RNKFCD DQTEGNKIKNRREEK HRCRGQSKLNIIIDNVVKA VNG GKSQREQA EFADCITFGIRHNTS PKMSRVRGGG/TPWAVLGMA EASSSLQSSSQNPQGAGWQTGP WV VSLGC
27831	58199	B	28001	1	2268	
27832	58200	A	28002	1	639	

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27803	58171	A	27973	1	2406	
27804	58172	A	27974	201	1069	
27805	58173	A	27975	450	647	
27806	58174	A	27976	329	697	
27807	58175	A	27977	141	1506	
27808	58176	A	27978	1	1773	
27809	58177	A	27979	3	460	PHRVMGVPISRGTL*SVFP*PS* CTTWPGSLGSCCTTACQVRCQPQ APHQP*APPERTTSAPAAQSPSR SSLWVTAPLVSACPTCSPATHP TRSQMPSTHTPCCRGSPPRGRS PSWTRTWTTCPKASKADPKAP WPCSLMPFYAQTQTLGET
27810	58178	A	27980	1	1803	MGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRE PTKWEKIFTTYSSDKGLISRIYN VLKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCS SLAIGEMQIKTTKKLMLYYDVI RICHDSHKELEQKLAFLGMED AILYSSCFDANGGLFETLLGAE DAIISDALNHASHIDGVRICKAK RYRYANNDMQELEAAYYRSTR PLSTRLFSFRSRVLTEFRVCPCL VHTTWGGNLMRLSARSLWQR AAVNIPKLEGIIIEY/ALLV/WR AML/TEVNLSPNPGLVDRINFG AHKDMALEDFHRSALAIQGWL PRFIEFGACSAEMAPEAVLHGL RPIGMACEGDMFRATAGVNTH KGSIFSLGLLCAAIGRLLQLNQP VTPTTVCSTAASFCRGLTDREL RTNNSQLTAGQRLYQQLGLTG ARGEAEAGYPLVINHALPHYLT LLDQGLDPELALLDLLLLMAI NGDTNVASRGEGGLRWLQRE AQTLQKGGIRTPADLDYLRQF DRDTSQGSSRVDCSVWELCRA GRTAGVMAVAAKTKNAGKWH NHIIRRFIDINPGDRLYDQGGRA HHPFAGTHHQKYRHRSR
27811	58179	A	27981	1	1974	
27812	58180	A	27982	344	508	
27813	58181	A	27983	3	492	
27814	58182	A	27984	65	261	

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27779	58147	A	27948	272	393	
27780	58148	A	27949	333	622	
27781	58149	A	27950	11	1850	
27782	58150	A	27951	1	1107	
27783	58151	A	27952	1	1348	
27784	58152	A	27953	3	431	KLQNELLLLHVSHPGHADAKG GFPWP*AAPPLWLCRVQPSFWL LSWAGIEGLWLFHTDHTSCQWI YHSGVALADVLHESPALQOTS VWTSRSFHTSSEIQAEVVPKPQLL TSVHAQAQYSMEAPKAWGLYP LKPWPELYLGPF
27785	58153	A	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGR SGKQSSGCHFWLLQHQICTCPS RVMGPRKKHRPTARGSRPPQPL PSGFPSAGAMGQVHCLAAPHS LERNRNPRTQ/PPGWEG/PPTR ANLALLPTPAATATNSSIPDSP PGSDGSVPAGLTTWLAVLTLD CPKAFGKVASQACLLWKGEQP PKTPPVTPSRVSLASEPNTIRL KNVFPRVFPACTWKSHRHSTPA HESSQKGLYPAKPQGWSCPRL WEPTSCISVTWM
27786	58154	A	27955	1	224	QWRHCNRSLPVQKGKSGALEG IGPPRVFAPPE*RAFGGQRAPPDI PAPPSPRHPTKDRRTAARSGPRR KRGQTNE
27787	58155	A	27956	681	879	LQISHPGHADASGGFPWPWAA PPLWLCRVQSPS*LSSQPGVECP QLFQAHSASRHLNSMRPQMNS S
27788	58156	A	27957	835	1482	
27789	58157	A	27959	1	522	
27790	58158	A	27960	2	396	
27791	58159	A	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	A	27963	370	3675	
27794	58162	A	27964	52	117	
27795	58163	A	27965	3	290	PRKTVQFGGTVTEVLLKYKTG ETNDFELLKNQLLDPAIRDD\QII NWLLEFRSSVMYLT\K\DFE\QLI SIILRLPWLNRSQ\TVVEEYLAF LGNLVSA
27796	58164	A	27966	1	2988	
27797	58165	A	27967	1	666	
27798	58166	A	27968	274	930	
27799	58167	C	27969	13	231	
27800	58168	A	27970	46	386	
27801	58169	A	27971	3	451	
27802	58170	A	27972	160	494	

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27762	58130	A	27931	128	586	
27763	58131	A	27932	271	465	HLTRPGTLLRQNFQRNDQAAT LA VHQYPLLCSNRC/CIPRQT/W VWSGPPANSNRPA AEGPDC*KE N
27764	58132	A	27933	1	375	MQKSPIFCVAHAGSCRLELFLF GHLGGHHPDTKPGRDTTRKDN FRPISLMNIDAKILNKILANRIQ QHIKKLIHRDQVGFISGVQGW NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQGFMLKI LNK LGIDGMYLKIIRAIYDKPTAKIIL NGQKLEVFLKGTGRQRCPLSP LLFNIELEVLARAIRQEKEIKGI QLGKEEVKLSLFAHDMIVYLEN PIVSPQNLLKLISNFSKVS GYKI NVQNSQAFLYSNNRQT*AIAGA PPASLPCCSLISDCCASNE*GSV GIGPSKPGAGYNLLLCHLISPSIS PTSSPKSDTCPIADFSNKSPDRSS AGDILLAMQSLGSM AIFTILILP THEHGMMFFHLFVSSFISLSSGL
27765	58133	A	27934	1	1059	
27766	58134	A	27935	1	533	LSKQGHNLNLRQFLLPFG\C*CLP LRGGVYRGRQ\ASLSCGGLHP V*AS\RQLCLPTQALA\MAGTPP PASLPCCSLISDCCASNERGSVG MGPSEPRCGNNLVVC\RFLSL SEKRSSIRVGVTFRFSRCHLSQL CLATKGNLSLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	A	27936	140	426	
27768	58136	A	27937	1	918	
27769	58137	A	27938	54	102	
27770	58138	C	27939	244	462	
27771	58139	A	27940	234	282	
27772	58140	A	27941	328	1212	
27773	58141	B	27942	245	338	
27774	58142	A	27943	483	635	
27775	58143	A	27944	9882	10134	
27776	58144	A	27945	2	370	
27777	58145	A	27946	1682	1945	
27778	58146	A	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE AEGEDCCCCCCCC\CCCCCCCCC CCCCCCCCCCCCCLPPSAGGRGP SGSARYFALIDAAQREDGGDA YRVGLAAALEVNAAETVACGG LEGGEAPTDAGTRYVLEPEAPQ LSVLWKRVEVQRLVPVRVVVA AWHAARKARAWLRRARP GP PASCALRRPSGYAAARN

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27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIPL LLLPSLSGDYETVRNGGLIFAG LAFIVGL\ILLSRRFRCGGTKKR RRINEDEP
27741	58109	A	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	A	27912	139	351	GGRRIETGGWERPPIPLLLPSLS GDYETVR\NGGL\IFAGLAFIVG\ LLILL\SRFRFCGGNKKRRQINE
27744	58112	A	27913	2	431	
27745	58113	A	27914	217	289	
27746	58114	A	27915	255	389	KPNACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRRTFLEEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMSGTAGRCKTLT EQ*LNTTATLCLLLREARKTL MTHQSTWTWMKLETHLSKLTQ EQKTKQRMFSLISGS
27748	58116	A	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	A	27919	54	320	
27751	58119	A	27920	443	477	
27752	58120	A	27921	1	963	
27753	58121	A	27922	1	2292	
27754	58122	A	27923	3	736	SCCLHSRLVRARRLRRAVAVM AAQCVRLARRSLPALALSVRPI FPGLLCTATK\QRTSAKNLKGD MGQSEQRADPPATEKTLL\EEK VKL\AEQKLVETVEKYKRALA\D TEELTGRGSQNLLREAKLLRHF KPFCKDLLLEVADVLEKATQCV PK\EEIKDDNPHLKNPLWRGLV MTEVQIQKVFTKHGLLKLNPV GAKFDPYEHEALFHTPVEGKEP GTVALVSKVG\YKLHGARTLRP ALVGVVKEA
27755	58123	A	27924	253	363	
27756	58124	A	27925	235	318	
27757	58125	A	27926	1	426	
27758	58126	A	27927	146	254	
27759	58127	A	27928	1	1401	
27760	58128	A	27929	61	457	LESTLATAERFLIPSPSTGN*L VCFCTT*GQECYSVTRF\SLGYG SPGCLYA*SSLIPCWRWGTPRL CCEKPFTHFCLRFVSPSKLAVS RWHIPLGSEEKRRSMSAGTISL HFIWMKSPTRTSFQHFCT
27761	58129	A	27930	1	567	

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27725	58093	A	27894	186	2192	QRRPRPFPSQGISMTECFLPPTSS PSEHRRVEHGSGLTRTPSSEEIS PTKFPGLVYRTGEPSPPHDILHEP PDVVSDEKDHGKKKGKFKKK EKRTGYAAFQEDSSGDEAESP SKMKRSKGIHVFKKPSFSKKKE KDFKIKEKPKEEKHKEEKHKEE KHKEKSKDLTAADVVKQWK EKKKKKKPIQEPEVPQIDVNL KPIFGIPLADAVERTMMYDGIR LPAVFRECIDYVEKYGMKCEGI YRVSGIKSKVDELKAAVDREES TNLEDYEPNTVASLLKQYLRLD PENLLTKELMPRFEEACGRTE TEKVQEFQRLLEKPECNYLLIS WLIVHMDHVIKLETKMNIQ NISIVLSPTVQISNRVLYVFFTH VQELFGNVVLKQVMKPLRWSN MATMPTLPETQAGIKEEIRRQE FLNCLHRDLQGGIKDLSKEER LWEVQRILTALKRKLREAKRQ ECETKIAQEIASLSKEDVSKEEM NENEEVINILLAQENEILTEQEE LLAMEQFLRRQIASEKEEIERLR AEIAEIQSRRQHGRTSEETEEYSSE SESESEDEEELQIILEDLQRQNE ELEIKNNHLNQAIHEEREAIHEL RVQLRLLQMQRAKAEQQAQE DEEPEWRGGAVQPPRDGVLEP KAAKEQPKAGKEPAKPSPSRDR
27726	58094	A	27895	12	413	PSRAPGLQKACTGHEGMAVHP PRIPVQSDHLISIEGLLCKLPCA GQVTKEGLVSFSLRPVLPQNT LSNSFYLFPGYASPYVETFLPG AHSGPAPPGLPVTRTPRTAKRL/G VAVAPSPTF*ISPRALRSTFVSN
27727	58095	A	27896	1	361	
27728	58096	A	27897	2	162	
27729	58097	A	27898	248	381	
27730	58098	A	27899	73	254	
27731	58099	A	27900	1	729	
27732	58100	A	27901	1	762	
27733	58101	A	27902	2	334	
27734	58102	A	27903	3	369	
27735	58103	A	27904	669	1006	
27736	58104	A	27905	3	250	
27737	58105	A	27906	721	876	
27738	58106	A	27907	3887	4013	
27739	58107	A	27908	3423	3627	



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27704	58072	A	27873	263	714	KLVNPIIKATNTIMNMTMNLK MSLTAPPSDICRGPKLSFAGKIQ AIEPKLKTATAQRPLDTIGLEV PVPAAWLLSAVRNCSKLRATS GPNLDTMNGSRRQTGSWTEGS RSSMKPHLLSDITGALR/SPKVS *AFCRLATWPFNFLQSGILS
27705	58073	A	27874	347	902	
27706	58074	A	27875	17	1178	
27707	58075	A	27876	1	1155	
27708	58076	A	27877	3	1109	EKETMQSLNDRLASYLDRVRS LETENRRLESKIREHLEKKGPQ VRDWSHYFKIIEDLRAQIFANT VDNARIVLQIDNARLAADDFRV KYETELAMRQSVENDIHGLRK VIDDTNITRLQLETEIEALKEEL LFMKNHEEEVKGLKTPNYA ALG*TVVDAPKSDLAKIM ADIR\AQ\YDELGSERTERKLDK YWSQQIEESTTVFTTQSAIEVGA AETNLHRSCLKRTVQSLDRPW TSMRNLKAQLGEQP*GEVEAPL RPTRWSQLNGILLHLES\ELAQT \RAEGQRQA\QEYEALLNIKVKL \EAEIATYRRLLEDGEDFNLGD ALDSSNSMQTIQKTTTRRIVDG KVVSETNDTKVLEALSQQKAG
27709	58077	A	27878	1	1305	
27710	58078	A	27879	209	560	
27711	58079	A	27880	219	512	
27712	58080	A	27881	528	803	
27713	58081	A	27882	3	432	SSPCVEFSTSMGACLRPATARSP SATCTAWTCTGWRRGRPWWR WTPENSGVAGGDTSEEDSEE VEGAEWGRRRRQRRGERCG GLRRAPCQGAPGKCLCPRPP\GP SPC*/CEALGAQRAS*PHRRELK VGGPGPGCELSPMV
27714	58082	A	27883	117	483	
27715	58083	A	27884	1	1497	
27716	58084	A	27885	228	776	
27717	58085	A	27886	1012	1677	
27718	58086	A	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	A	27893	1	1692	

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27694	58062	A	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKTSRRQEITKIRAEKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIGN DKGDIITDPTEIQTIREYYKHL YGNKLENL*H*MPRESRKDLK LTP*HHN*KN*RSKSKHIQKLAE GKK*LRSEQN*RK*RHKKPFKK SMNAGAGFLKRSTKLIDR
27696	58064	A	27865	1	1920	
27697	58065	A	27866	444	763	
27698	58066	A	27867	1	651	
27699	58067	A	27868	94	964	VNADWVLQRELEQTSWSSKQ RACCLSHVVGRLMISSCTTRKM AEEEQRKIPLVPENLLKKRKAY QALKATQAKQALFGKEGAEER KRAQ/WFKRLESFLHDSLAAET *QG/RISRQLEVQPHALELPDKC SLAFVVRIDGGSLVQRTIA RLCLKKIFSGVFVKAPPRIQKW LRIVEPYVTWGFNPKSVRELIL KRGQAKVKNKTIPLTDITVME EHLGKFGVICLEDLIHEIAFPK HFQEISWVLRPFHLSVAHHATK NRVGFLKEMGTGGRGERINQ LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLLSIMAALRPLV KPKIVKKRTKKFIRHQSDRYVK IKRNWRKPRGIDNRVRRRFKGQ ILMPNIGYGSNNKTKHMLPSGF RKFLVHNVKELEVLLMCNKSY CAEIAHNVSSKNRKAIVERAA QLAIRVTNPNAARLRSEENE
27702	58070	A	27871	2	423	
27703	58071	B	27872	193	1698	

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27674	58042	A	27843	37	299	ILLCSVQTLPLLRREFYGHIPKC QQSLNIICSPSSLRIPGFLHRNRL STPFHVQQPQREHF*YCRSQIH GENSAWHIRSHHAEKAHF
27675	58043	A	27844	84	428	PAEIERSTAKTPGPPGSLEMGLL TFRDVAIEFSLEEWQCLDTAQR NLYKNVILENYRNLVFLGIAVS KQDLITCLEQEKEPLTVKRHEM VNEPTGPRQKRRVTSSR**MKR YVII
27676	58044	A	27845	1	719	
27677	58045	A	27846	669	830	CLVQNNQIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHW
27678	58046	A	27847	223	382	CLVQNNQIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHW
27679	58047	B	27848	1	491	
27680	58048	A	27849	1	1113	
27681	58049	A	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM FRRIKDALFRTIQFCQIMNRSQ YMFTCRCRTEMQVPQHRRKKT FKPTVLLNHFVMEIIVLTAGRID AAFQDEVAASEGFLKQPVGKD YKFGGSPVKDEKLFGVGTGMG HHN*LSV*TSIQHLLSNTQG/CL RVCPALRL/HSRNL SAMVISFSF SCGARS AISPINARKRWASPVC
27682	58050	A	27851	1	2697	
27683	58051	A	27852	1	1998	
27684	58052	A	27853	864	1025	CLVQNNQIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHW
27685	58053	A	27854	1605	1766	CLVQNNQIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHW
27686	58054	A	27855	677	735	
27687	58055	A	27856	1126	1568	SSSSTGRSRHKEVSPGCQQDGL RCQEWWSVRPG\YEATGGVWG KQLGIPASGLPGRRSSESPRKSC TPVTSRTGLPVC PWAALSPESR SFSLSVRPVCVC\CVGTKMSCA PECCFFLVSLSLSLFLRLLLGL AAHCQFFPAVPLCIL
27688	58056	A	27857	1142	2450	
27689	58057	A	27858	1	1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	
27692	58060	A	27861	1	657	
27693	58061	A	27862	248	382	QPPKITLLYQQWIQTKKSLKS FLP*QEFRKMQKKHSTKSSITL

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27656	58024	A	27825	44	621	
27657	58025	A	27826	406	727	
27658	58026	A	27827	2	1337	
27659	58027	A	27828	1236	1391	
27660	58028	A	27829	228	502	
27661	58029	A	27830	1	1035	
27662	58030	A	27831	146	392	GHRSHQSPEETPNLIPRTPIPLG TGTSIRSTRIPRTEASGPNGLN WYLTPTPGGQRPSAASPRGF PPTNNSRLPAEPE
27663	58031	A	27832	15	300	
27664	58032	C	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVRVPG GSGGLRHWCPGGLGRGLGQA PEHKVRLSMEFCSTCTADHISLS SFWRSSFQQPLVPAVSLQSPDR RLSHDPAASSWSGFCGISPAFSA FSECPSSLRSHPPALLQAAES* FAASSPSPTWSLSGSGTRKPW S/VACNWLLSDSSSHRRSFWES GIITMVLALTLEELV
27666	58034	A	27835	1	231	DELLVGGNPRGDAAEEGRCP GGVGVRYQIQIWPRLCSRNP GAAD*GPGS*RWDRCPRDEIWR FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESEGE AQALVPSVAS*/SSRPWDRPPST K*GCLWSSAARAQQTIIHVS GGHPSSSHWLPAVSLQSPDRRL SHDPAASSWSGFCGISPAFSA ECSPSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPPAPCLLAGLLCTCC RTP*TASLCARGPVPRPRA*EAT RG TSA*ALHSPPGTLTPTVTRTS PSHLSARAAAPSHPARPTASRSS RLPAWLAVRLSIPPRRGS LGGA GAQAAAASTRFTCCS
27669	58037	A	27838	1	211	ATALAERWLGEVLVRVGVRVP CGEWRAQALVPIVAS*ATRPSG RGPPTQQT*RTSRIGRS*QTTMR HART
27670	58038	A	27839	316	537	
27671	58039	A	27840	255	475	RPWVRAPYKLLPALLHAPLCAP PSSPWRPV/PASAPSFKLLKS*IF CKQLSLLPTWSLSGSGTRKPWS GPVTGS
27672	58040	A	27841	622	1127	
27673	58041	A	27842	364	666	

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27639	58007	A	27808	126	893	EDGSGGGKFPEGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPRGGT RGQEPQMKETIMNQEKTHTC RHKVRJGGKGTARKKKKVVHI TATA\DDKKLQFLLKGS*GVN NISGIEVNMFTNPRNKLIHF*Q PLKVQGISWAANTFHHLQGHA *DKSSWTEMLPSIFKPSLGAG*V *LVLRRLA\EALPQTNLWDGKS TLLLLGEDDGD\DESSQILWEY FGWRVPRNEANLNLSTF
27640	58008	A	27809	180	589	KELPLLIFCRWQFESLHENVPF FKVGSBDTNNFPYLEKTAKKG SPNGDLPVGCKSNGHP*SKFIRS VKPLNPQLLASLQCTSAAYPLQP EDVNLRVISVSRRREGVPFLGHL LWGRSLFYNQNSNKHGILYN
27641	58009	A	27810	623	1082	
27642	58010	A	27811	548	645	
27643	58011	A	27812	329	510	
27644	58012	A	27813	3254	3628	
27645	58013	A	27814	1	960	
27646	58014	A	27815	349	681	PMASNRAITLTAWPKIPFLGICE AKNPRSENMR\AAHFGSGLPP SWELWEQGPPGNSSRYIEFLNK HTYIKGTLRVYTKKFCMLVIKS FESKSCVWRYDFDSKSSVNVTV
27647	58015	A	27816	240	473	
27648	58016	A	27817	825	1043	
27649	58017	A	27818	2	418	GKVVCFEAFLOQILGKHQFYW CLEGLGHCHHHIGAKYPEDIVD EESAQQDAASADIVEVQELYSI KGEGQAKKVVGPNVLPQQVPD ANDAAQAQAHQVLGVKFIIDD L*AERPGKSTP*GRATPPTFLVF PRTLCEGI
27650	58018	A	27819	2	427	
27651	58019	B	27820	51	672	
27652	58020	A	27821	43	667	
27653	58021	A	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL HLRCLLGIWHQCDGDSGQVLR GTNENLVFPQDLLEKGLEANNF AMLGTWEMSSFGIFIALLLRF DISLKKNTHTYFYTSFAAYIFGL GLTIFIMHIFKHAQL*GVKS*GS SGSDRIQRGNRGISIEGAGEERE MMQLVPEPLRARPDRLWGLGPH RRA
27654	58022	A	27823	1	1019	
27655	58023	A	27824	1061	1258	

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27629	57997	A	27798	1	629	MKVGLDQIIEVVP SHSVTSGAA AGECGGVHCD SVCAEGRWGP N CSLPCYCKNGASCSPDDGICEC APGFRGTTCQRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNE/RLFTVCPSGR FGKNCAGICTCTNNGTCNPIDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTCQCEPGWGGTN CSSVKKQSTVCES
27630	57998	A	27799	108	1071	YPLFLSSISACDGDHWGPHCTS RCQCKNGALCN PITGACHCAA GFRGWRCEDRCEQGTYGNDCH QRCQCQNGATCDHVTGECRCP PGYTGAFCEDLCP PGKHGPQCE QRCPCQNGGVCHHVTGECSCP SGWMLSFP GWRPI*FSKSL*MQ GTVCGQPCPEGRFGKNCSQECQ CHNGGTCDAA TGQCHCSPGYT GERAAVPDVRK\ CQDECPVGTY GVLCAETCQCVN GGKCYHVS ACLCEAGFAGERCEARLCPEGL YGIKCDKRCPCHLENTHSISLIA AKKSNSLHAIALDFRAQCQSVK DRCHASDLPI DIVSTETLR
27631	57999	A	27800	243	1296	ETQEESEFLPCGSHQPNG*LLF CSTYKRCLCNWGPC*AY*RACP CPALQQCPDI/CPQAQLAIPCAP QQQQLSRCLSFPSLLQDPNTP G/EYRKDEGRAGSRGAGEKQC THNSPRWLQNTVSNQGSSMPG FQSHVPSLLGAFVQCTNCTRV SSPANKIFTTFR LGDPLVSPCHQ GFGSNTHCCVESWQSSCSGMH KDLGALHTPAPGSPTNVAATQ ARREPRCRLAVLSTLDRSTRQK VNKDIQELNSALHQADLTDIYR TLHPKSTEYTF FSEPRTYSKTD HLVGSKGLLSKCKRTEITNCLS DHSAIKLELRIKKLTQNCSTTW KLNNLLLNDY WWHNEMKAEID
27632	58000	A	27801	552	827	
27633	58001	A	27802	70	200	
27634	58002	A	27803	18	1057	
27635	58003	A	27804	652	960	
27636	58004	A	27805	1	474	
27637	58005	A	27806	1	140	
27638	58006	A	27807	1	1260	

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27609	57977	A	27775	3	197	RPDAVPARSLEMKRFPMPPPP\G*FSPGASLDVNP GCYKQAPSCSLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFSGGLGCQH*RRSPLHEHPSSGP\ PAGLKPSLSCLPAGQGSGPAARY/GLSLPPTPWAPVQPEPPRRAPPPAPGRSVPSTTQGLRSASA
27611	57979	A	27777	177	444	RGGQSGSPAACYA*/RLPPTPWAPVRPEPPQRAPPPAPRRPVPSTTQGLRSASTRRVTGRQLHLQPWCGIHWVKPAGLLSLVGRWRV LMS
27612	57980	A	27778	165	591	QRAGSPHSRSL SAPPLPGLPLWRHLRSPSAHRCTVRAPFWAGQGRSRLPQLAGRCGGRGASGNPGVSHGACGPAGVPGGRGLGGPRTGSSQLALPAPGNEGLSTPASGRRKKLRTHPSIRRNKLQTRYLKSCNTHREGPRLH
27613	57981	A	27779	1	1605	
27614	57982	A	27780	2	1970	
27615	57983	A	27781	1	3522	
27616	57984	C	27782	183	254	
27617	57985	A	27783	39	346	QYISELQFLASTVRQTPATSPAHKNFQTPEPQQPGIPPEPPPPGACYKCWKS GHQAKECLQPGIPRK/HASHLWQPLPEPPGT LAQGS LTDSFPDLLGLAAED
27618	57986	A	27784	1	354	
27619	57987	A	27785	72	299	
27620	57988	A	27786	273	530	LGSGDLPWGINPLSSCSLLREKDPLTISGPQTHQPKHLTNFKSGPH*KSDCSTAPGATPRAPGT LAQGALTDSFPDLLSLAAED
27621	57989	A	27790	1	1068	
27622	57990	A	27791	148	527	
27623	57991	A	27792	2	1910	
27624	57992	A	27793	1	1047	
27625	57993	A	27794	96	488	WDRMAGGSSNTFGFPPPLPYRSCER*QRDGGPRSPGSLSVPPWPR/PPILAALEEPFSPPLHRGRPSLGWPRPELAPSAQRSAAS/RPEASKDHEPTRKKE/PTPDTQP*EL*HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	A	27796	3	412	
27628	57996	A	27797	2	390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27599	57967	A	27765	1	927	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRLPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHR\IIPGFM\CGQ\GD FTPP*MAPGGKSIYGEK\FEDEN FILKHTGPGILSMANAGPNTN GSQFFICTAKTEWLDGKPVVF GK\VKKGLNIVEAMERFGSRNG KTSKKITIADCGQLLISFDLCFIL NHQDHSFCALLSGEHPSTPFAR RILRILWLSLQFLWGSMSLFPF MPSWIAAVKFMIIIEIKTK
27600	57968	A	27766	1	798	
27601	57969	A	27767	1	575	PTRPPTRPPTRPIMAQDQGEKE NPMRELRIKRLCLNICVGESGD RLTRAAKVLEQLTGQTPVFSKA \RYTVRSFGIRRNEKIAVHCTVR GAKAEIELEKGLKVREYELRKN NFSDTGNFGFGMQDHIDLGIIY DPSIGIYGLDFYVVLGRPGFSIA DKKRRTGCIGAKHRISKEEAMR WFQQKYDGILPGK
27602	57970	A	27768	1	1695	
27603	57971	A	27769	1	228	
27604	57972	A	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT APV/VSGGSHDHIQQYSDIEDFR QATAASSVMVARAAMWNPSIF LKEGLRPLEEVMQKYIRYGGM GAALLSDPDKIEKAPSMGTLM GVYLPCLQNIFGVILFLRLTWM VGTAGVLQALLIVLICCCCTL TAISMSAIATNGVVPGYLHTLV QNLVNNGYVRDETVRAAPYD WRLEPGQQEEYYRKLGLVEE MHAAYGKPVFLIGHSLGCLHLL YFLLRQPQAWKDRFIDGFISLG APWGGSIKPMLVLASGSGTRA
27605	57973	A	27771	1	1710	
27606	57974	A	27772	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL RSPSAHRCTVGAPFWAGEGRSP LPQLAGRCGRRASGNRGVARG ACGPAGVPGGRGLGGPALGAA GRPGP*LPSRGAGLGTA/GPPCL SLPPPPWVPVQPEPPRRAPPPAP RRPVPSTAQGLRSASA



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27580	57948	A	27746	166	405	RPRSERLLWGTSPLS/CALT*G DPPTTSGPQTNQPRNISPISNRD PTGKWTVQLTRQPLPELELWP KALRLTPSQIFSA
27581	57949	A	27747	425	484	
27582	57950	A	27748	448	520	
27583	57951	A	27749	3	679	GGGFSDRDRTIALQPGQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTPDPGAHRNPS GGYSATDCEGSRPAEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLREKD PPTTSGPQTTSRPNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP EPELELWPKAL
27584	57952	A	27750	3618	3848	NLCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSR*REESTS LHDPMASSSSTVFWGLKRQKY FLWPFRAS
27585	57953	A	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPAPV PQSPLKNELRRKYLT
27587	57955	A	27753	1993	2205	
27588	57956	A	27754	138	833	
27589	57957	A	27755	1	875	
27590	57958	A	27756	1	1041	
27591	57959	A	27757	3	1447	
27592	57960	A	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTSSPSIW AAWRPPT*LTVTSRPGTSGSE PWAMAAASRWQ
27594	57962	A	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRRKPHGHQKSL PASLRFPGR*TPQPDLPGPPAQ PAQGPQAATVPGRW
27596	57964	A	27762	1	280	
27597	57965	A	27763	1	714	
27598	57966	A	27764	2	558	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKAVNFA DAAAAQGPLLAMVNPTMFFH IAVDGEPLGCVSFVIRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFYKGSFCF RIIPGFTCSGDFTRHT/GIGGKS ICREKFDDKNFILKHTGPGILSM ANAGPSVNV

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27556	57924	A	27722	1	2373	
27557	57925	A	27723	2	272	RARTPPLWPRARGPGSRVSGAP WFLDLAAGGGFLPPAVLCDLSA ASSTVSGRSNPHC*AWGGLEFF GEVERAESGFPVPEPSLISEMPH
27558	57926	A	27724	195	489	
27559	57927	A	27725	210	1308	
27560	57928	A	27726	203	474	
27561	57929	A	27727	224	892	
27562	57930	A	27728	1	457	
27563	57931	A	27729	3	1325	
27564	57932	A	27730	322	512	
27565	57933	A	27731	621	737	
27566	57934	A	27732	441	588	
27567	57935	A	27733	1	792	
27568	57936	A	27734	8	488	SGCRNSARADADPSLHASPPAP TMATVQLLEGRWRLVDS\KGF DEYMKEVLGVGIALRKMGVAMP KP\DCIITCDGKNLT\IKTESTLK TTQFSCTLGEKFEETTADGRKT QTVCNFTDGALVQHQEWGK ESTITRKLKDGKLVVECVMMN VTCTRIYEKVE
27569	57937	A	27735	861	2161	
27570	57938	A	27736	349	625	
27571	57939	A	27737	1	630	MAQETNHSQVPMCLCSTGCGFY GNPRTNGMCSVCYKEHLQRQN SSNGRISPPATSVSSLSESLPVQC TDGSVPEAQSA LDSTSSSMQPS PCIK\QSLLSESVASSQLDSTSV KAVPETEDVQASVSDTAQQPSE EQSKSLEKPKQKKNRCFMCRK KVGLTGFEFCRCGNVSCES\HRY SDVHNCSYNYKADAAEEN/LE KENPVVVGEKIQKI
27572	57940	A	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLEGIVNISPQ*S VRKGHFDTL SKG\ELKQLLTKE LANT\IKNIKDKAVIDEIFAQGLD ANQDE\QVDFQEFISLVIAIALK AAHYHHTKE
27574	57942	A	27740	1	519	
27575	57943	A	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	A	27743	619	890	
27578	57946	A	27744	113	328	LGSGAWGGGDLPWEINPLSSCS LLREKDLLTTS GPQT\TS PRNISP ILNRDPTVQLTWQPLPEPLELW PKAL
27579	57947	A	27745	501	680	

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27543	57911	A	27709	3	959	MANNPGANGQ\PGGPGGPGMG KPRCF\RGEVFGIVIRGRGSRP/R GRGRGR\VRGARGSKGRG*RE WNAVHQVGAALVKDH*RSKFP WKEIYLFSLPH*RNQRIIDF\FLG GLLSKDEGFE*LCPVQKQTRA\ GQPHPGFKA\FVAIGDYNGHV GLG\VKCSKE\ATGHPVGAIIL AKLSIRPRCAEGYLGKLVAKP \HTVPLQGDKGRCG\SVLVRLH PLHPRG\TG\VSAPVA\KKLLM MA\GIDDCYTLS\ARGCTATLG QIWPRAT\FDAISKTYKLP*PPD LWKETVFTKV\PYQ\EF\DLV KDPHPRESSVQQDSELQLVATT
27544	57912	B	27710	50	1598	
27545	57913	A	27711	1	3916	
27546	57914	A	27712	334	462	PAFITVNCSSARKLIQV*GPVA CRVHILPLVVRCPKPGTTG
27547	57915	A	27713	256	654	
27548	57916	A	27714	1	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSSELQPTASSSSA RSSPSPASQVPPGPAGAAAAP HPPCCPESTCWTWPC*SPLCH WAVA*ARSGPGLGECFETHGP HGCPPGQSPRPQ*APSAWTE VQPR*PRPAPEGSSRRPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAPKCTSGPPHVRV AQPQDDAPREEPPYLPNGMPPG RDAPHLDPWAASQRGSSHPRR WPPSQRRSLLPRRVADRPEAAI SALWEAKAGGWETLPEMEITIH NKTRQSKRITHQTNRPNTSSKTI RITKTDLTSWETQSPGSPDRHR KPSTATKHNRFSKIYSRFSIFQC DQGLNGRCGQKGAGKEQRM QEQQENFQAPPFQSHPALRSLQ MQQVQTEEHFGTLECGKLAQC SFHPTREEDRNQDGKTDMLHF KLELPLQSTEHLVGLVQLILTFY RLHSCGIPSVLSRYPYFSMLAFG ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGLGECFETHGPHGCPP GQSPRPQ*APSAWTEVQPR* PRPAPEGSSRRPPPGAPCPAQ PTRRCPRHQTPPAAGAAVP
27554	57922	A	27720	507	1114	
27555	57923	C	27721	80	223	

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27537	57905	A	27703	717	1803	STGRKAPHHTYSKIDHILGSKA LPSKCKRT/E/IITNCLSDHSAIKL ELRIKKPTQNPSTTWKLNLLL NDYWVNKEMKSEIKMFFETNE NKNTTYQNLWDAFKAVCRGK FIALNAHKGKQERSKIDTLTSQ LRELEKQEOTHSKVSRREQITKI RAEPKEIETQKTLQKINESRSWF FERINKIDRRRLARLIKKKREKNQ RDAIKNDEGDITDPTEIQTIR EYYKHL YANKLENLKEMDKFL NTYTLPRLNQEEAESLNRPIAGS EIVAIINSLPTKKSPGPDGFTAEF YQRYKEKLVFGAGYFGMWAL AALPSNLLKLSQLCQEAEEVNV LVQFVCICPAQEPTIDVLFSLV PPLSLILN
27538	57906	A	27704	407	1696	NILRNAVPHQQQNK A*RRMTL TS*EKKASDDQTPSYRRKFKA KAKKLNT/YEKNLDECITRITNR EKCLKELMELKAKARELREEC RSLRSQCDRLEERVSVMEDEM NEMKREGKFREKGIKRNEQSL QEIWDYVKRPNLHLIGVPESDR ENGTKLENTLQDIIQENFPNLAR QANIQIQEIQRMPQRYSSRRATP RHIIVRYTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLLAET LQARREWGPIFNILKEKNFQPRI SYPDKLRFISEGEIKYFTDKQML RDFVTTRPALIEALKEVLNMER NNRSPSSSPATEQSWMENDFDE LREEGFRRSNYSELREDIQTGK KEVENFEKNLEECITRITNTEKC LKELMELKTKARELREECRLR SRCDQLEERVSA MEDEM NEMK REGKFREKNKKK
27539	57907	A	27705	2597	5904	
27540	57908	A	27706	1	675	
27541	57909	C	27707	137	1357	
27542	57910	A	27708	1	1032	

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27535	57903	A	27701	1	2231	MGKKQSRKTCNSKKQSASPPP KERSSTPATEQSWSENFDEL EEGFRRSNYSKLQEEIQTGKE VKHFEKNLDECITRITNREKCL KELMELKAKARELREECRLRS QCDQVEERTLARLIKKKREKN QIDAIDKIDKGDITTNPTETQT EYYKHLTYTNKLENLEEMDKFL DTYTLPRLNQDDVESLNRPTG SEIEAINHSLPTKKSPGDRFTA KFYQSLPSSCDYGHAPHPDVF RVSSFWVVRGLAGSGVKLQTF AVSVTALKAAARLELFIPDGA QLASPSGSLTRTGGGAACQSHA VCPHSSAFGWSMGLGAMEQG AALIGEARASREPMEEVGGSG MAACRSQALPRGQLRPSEKSR APEHSSSPAMEQSWMENDFDE LREEGFRRSNYSELREDIQTG KEVENFEKNLEECITRITNTEK LKELMELKTKARELREECRLR SRCQLEERVVSAMEDENEMK QEGKFREKRIKRNEQSLQEIWD YVKRPNLHLIGVPESDGENGTK LENTLQDIIQENFPNLARQANI IQEIQRTPQTYSSRRATPRHIV FTKVEMKEKMLRAAREKGDSV ERSFSNKAELLFQLHGHQRESL SKKEAQVWRDKGLYFRKGLLD QAQSWSRQVASILGAQIQVEGS PEQRLENVELAGGHLNTLKAIP MVAVAGGISFKCGAVLLLGAA
27536	57904	A	27702	596	1593	KPRLNENYVKNAEASGANAINW KKGYLVMEDENEMKQEGKF REKRLKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTKLENT LQDIIQENFPNLARQATVHIREI QRTPQRFSLRRSTPRHIVRFSKV ETKEKMLRAAREKEIQTIREY YKHLTYTNKLENLEEMEKFLDT YTLPRLNQKEVESMKRPITSSEI EAVINILPIKRSPGPDGLTATFY QRYKEELERSSSPATEQSWMEN DFDELREEGFRRSNYSELREDIQ TKVKEVENFEKNLEECITRITNT EKCLKELMELKTKARELREECRL SLRSRCDQLEERVVSAMEDEN

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27531	57899	A	27697	1	1783	MGARAGGSCSCLMWLLLASG HFMGCVAAGDTVGPKEFRSCY TITLLQSKLSYSFGKNNKNFQL RKCLQTVDNLFVPNQNGYYCH SQTSLDRAQIDLNGRIRNGSVY SAHSTNSLNNPQPYLQSPMSS NPSITGSDVMRPDYLP SHRSA VIPPSYRPTPDYETVMKQLNRG LVHAERQSHSLRNLNIGSSYAY SRPAALVYSQPEIREHAQLPSPA AAHCPFSLSYSFHSPSPYPYPAE RRPVVGA VSVPELTNAQLQAQ DYPSPNIMRTQVYRPPPPYPPPR PANSTPDL SRHLYISSSNPDLITR RVHHSVQTFQEDSLPVAHSLQE ERSSSPATEQSWTENDFDELRE EGFRRSNYSELREDIQTGKEV ENFEKSLEECITRITNTEKYLKE LMELKTKARELCEECSLRSQC DQLEERV SAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLAKQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGRVT LKG/ITHQT/RQRISRQKLYKPEE SGGQYSTFLKKRIFNPEFHIQPN
27532	57900	A	27698	3	1046	
27533	57901	A	27699	1	3585	
27534	57902	A	27700	937	1119	

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27524	57892	A	27690	1	1902	MNAKALPTLSPLPQATTESVSL TQERSSSPATEQSWTENDFDEL REEGFRRSNYSELREDIRTKGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVVSAMEDEMNEK REGKFREKRIKRNEQSLQEIWD YVKRPNVRLIGVPESHGENGTK LENTLQDIIQENFPNLARQANIQ IQEIQRTPQRYSSRRATPRHIIVR FTKVEMKERMLRAAREKEIQT TIREYYKHLIYANKLENLEEMD KFLDTYTLRRLNQEEVESLNRP TGAGIEAIINSLPTKKIPGPDGFT AEFYQRYKEELRIKYLGIQFTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEPSEI MPHIYNYLIFDKPEKNKQRGKD SLFNKWCWENWLAICRKLKLD PFLTPTKINSRWIKDLNVRPKT IKTLEENLGITIQDIDMGKDFMS KTPKAMATKAKIDKWDLIKLK ELLTAKETTIRVNRQPTKWEKI FTTYSSDKGLISRIYNEL/KQIYK KKTNNPIKKWAKDM
27525	57893	A	27691	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEKN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDL
27526	57894	B	27692	1	756	
27527	57895	B	27693	1	1743	
27528	57896	A	27694	1	1407	
27529	57897	A	27695	3	391	
27530	57898	A	27696	604	955	SSVFLGDPPIILIGNKEMCLSSVL LINGSINFLHPFREDKGAVDVP GVATQQILLNDPVLTAISEILG\ LVSSLSK*TSPPIPGPGGNA*AR QPSCP*KGELSWRSAPSLVQFSS

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27523	57891	A	27689	1	1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNRHEHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRLRSRCDQLEERR KQERSKIDTLTSQKLEKQEQ THSKAGRRQEITKIRAELEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTIEIQTIREYYKHLA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPIGSEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL HINRAKDKNHMIISIDAEKAFD KIQQPFMLKTLNKLVEVLARA IRQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP



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27515	57883	A	27681	1	1677	MARKDLPPAYGGWQVLDATP QEMSNGVYCCGPASVRAIKEG EVDLNYDTPFVFSMVNADCMS WLVQGGKEQKLHQDTSSVGNF ISTKSIQSDERDDITENKYEEE HFEAFQSVAQLPITRPFWSILRP F*RP*RKISTSFIRPLFTFL/LRLM NAHPEFRMAMKDAKTPGKIS YSQDSQDLSTDKLIRISALGEEK SSPEKILVNKIITLSYPSITINLLA RVLSPSLPGPAGLASRSEYGPA KPTPTGNSSWPASAARSPGSRP CLSLHTSPQAEGAGSGLDQPRE RLPQCSGELKGSSSAARMGAE NEEAPRASEGCQGCQQA VTSQ QDGGPLLQNRFFWDCGDENGA DAVYLDSEPQRQEYVMNDYGF IYQGSKNWIRPCPWNYGQAASP WRYGQWWVFAAVMCTALGIK SCDFQAARNNEEHHTKALSSRR LFVRRGQPFTIILYFRAPVRAFL PALKKANKGKLESFSYICFFSIV FGSKNSYAKVAYLEVAYPATL QNGALRKYLVLGA AVVNQPLS IQVIFSNPLSEQVEDCVLTVEGS GLFKKQKQVLIP
27516	57884	A	27682	1	1653	
27517	57885	A	27683	3	2170	
27518	57886	A	27684	2	244	ACPSTSTSHCRGATCSCSRTS\C SGVLQHSLRHCA SGRGFSSRCP ACCGSPGLGLPAALPPAAWGL QIAPSPQGTPGNSQS
27519	57887	A	27685	618	851	
27520	57888	A	27686	78	240	
27521	57889	A	27687	860	1246	
27522	57890	B	27688	1	2301	

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27512	57880	A	27678	3	1923	ATMAQGLEVALTDLQSSRNNV RHHTEEITVDHLLVRRGQAFNL TLYFRNRSFQPLDNIIFVVETE DAVYLDSEPQRQEYVMNDYGF IYQGSKNWIRPCPWNYGQFED KIIDICLKLLDKSLHFQTDPA TD CALRGSPVYVSRVVCAMINSN DDNGVLNGNWSENYTDGANP AEWTGSVAILKQWNATGCQPV RYGQCWVFAAVMCTVMRCLG IPTRVITNFDSGHDTDGNIIDE YYDNTGRILGNKKKDTIWNFH VWNECWMARKDLPPAYGGWQ VLDATPQEMSNGVYCCGPASV RAIKEGEVDLNYDTPFVFSMVN ADCMSWL VQGGKEQKLHQDT SSVGNFISTKSIQSDERDDITEN YKYEEGSLQERQVFLKALQKL KARSFHGSQRGAELQPSRPTSL SQDSPRSLHTPSLRPSDVVQVSL KFKLLDPPNMGQDICFVLLALN MSSQFKDLKVNLSAQSLLDHG SPLSPFWQDTAFITLSPKEAKTY PCKISYSQYSQYLSTDKLIRISA LGEEKSSPEKILVNKIITLSYPSI TINVLGAAVVNQPLSIQVIFSNP LSEQVEDCVLTVEGSGLFKKQQ KVFLGVLKPQHQASIILETVPFK SGQRQIQANMRSNKFCDIKGY
27513	57881	A	27679	1	756	
27514	57882	A	27680	1	2601	

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27507	57875	A	27673	3	938	MANNPGANGQ\PGGPGGPGMG KPRCF\RGEVFGIVIRGRGSRP/R GRGRGR\RGARGSKGRG*RD WVPVHQVGAALVKDH*RSKF PWKEIYLFSLPH\IKESIIDF\FL GGLLSKDEGFE*LCPVQE\TRA GPAATR\FKAFCCYPGTTNGHV G\LGVKCSQE\VAHRPFRGAIL AKL\SIVPVR\RGYWGNKIRKP\ HTVP\CKVT\GRCGSVLVRLIP/S QPRGTGIVSAPVPNK\LMAG IDDCYT\SARG\CTATLG\NFAK AT\FD\AISKTYSYLTPDLWKET VFTKSPYQEFTDQLVKDHTRVS VQRTQAPAVATT
27508	57876	A	27674	1	864	
27509	57877	A	27675	2	752	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFFKKKAVNFA DAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFMCGGDCE/RHHNGTG GKSIYTEKFEDENFILKHTGPGI LSMANAGPNTNGSQFFICTAKT EWLDGKHVLFKGKVEGTNIVE AMERFGSRNGKTSKKITIADCG QLLISLTCVLS
27510	57878	A	27676	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCGVEALTTLEVAGRM LGGVAKQEKKKKKTGRAKRRM QYNRRFVNVPFTFGKKKGPN
27511	57879	A	27677	567	838	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27478	57846	A	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA GRRSALCSRGLGP*RPPTRS GAAPGPHSPCGRPDGAPCSRLP PHRSRSPPHGSHVPAAGWLSAG PHQRWPA AAAAGPGTDQCRVVG PERASPHIWKGSTVPFLPSWTFL RVLSVPGCSLPRCCWLGHQC
27479	57847	A	27644	2	159	
27480	57848	A	27645	1	243	
27481	57849	A	27646	219	462	
27482	57850	A	27647	256	427	
27483	57851	A	27648	1	954	
27484	57852	A	27649	2	4690	
27485	57853	A	27650	1	1275	
27486	57854	A	27651	1	867	
27487	57855	A	27652	1	472	
27488	57856	A	27653	2	1215	
27489	57857	A	27654	3	401	
27490	57858	A	27655	712	1245	
27491	57859	A	27656	2	1178	
27492	57860	A	27657	278	339	
27493	57861	A	27658	1	1407	
27494	57862	A	27659	1	687	
27495	57863	A	27660	484	776	
27496	57864	A	27661	299	1318	
27497	57865	A	27662	1	960	
27498	57866	A	27663	122	282	
27499	57867	A	27664	1	600	
27500	57868	B	27665	1	375	
27501	57869	A	27667	356	439	
27502	57870	A	27668	49	360	
27503	57871	A	27669	2	580	GRVCGGPWAARVGERIPNMA GRKLAS*KPTD*VAFARD/IIPQ NPKAPLPSFLKS\WNGDPSPSRL\ AALP*ESHPA\IDWA*LPRPNVA QGLAWVDDFE\KKFNAAERFPC PEDK\YTAQVDA\EEK\EDVKSL C/AEWVSLSKA\RIVEYEKEME KMKNLIP\FDQMT\IEDLNEAFP ETKLDKKKYPYWAHQPIENL
27504	57872	A	27670	1	675	
27505	57873	C	27671	137	1357	
27506	57874	A	27672	1	1032	

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27468	57836	A	27633	108	441	
27469	57837	C	27634	156	287	
27470	57838	A	27635	2	363	RFTKVEMKEKIMLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL
27471	57839	A	27636	2	367	
27472	57840	A	27637	1	936	
27473	57841	A	27638	1	865	
27474	57842	A	27639	1	1287	
27475	57843	A	27640	1	2565	MGP GARLAALLAVLALGTGDP ERAAARGDTFSALT S VARALAP ERRLLGLLRRYL R GEEARLRDL TRCNDETITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLSRWAVGGATG SWVLSKGDRA SLGERVVTGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLSPSTRQRGQ SERSQDANGRRKQKTKSEPERF EDAVLLAGFKVEEPPVQRPRRK EWFQGPSPGHCCPAQPQDSAPC ILATHAPARAQNA PGTA WAAA LEGTSTVSLDHFHVVG VVVVS GGEIILL SFRFYDKVLSLHEDS TTPVANPLLAFTLIKRLQSDWR NVVHSLEASENIRALKDGYEKV EQDLPAFEDLEGAARALMRLQ DVYMLNVKGLARGVFQRVTGS AITDLYSPKRLFSLTGDDCFQV GKVAYDMGDYYHAIPWLEEA VSLFRGSYGEWKTEDEASLED ALDHLAFAYFREQSSSPATEQS WMENDFDELREEGFRRSNYSE LQEEIRTNGKEVKSF EKKLDEW ITRITNAEKSLKDL MELKTKAR ELRDECRSLSSRCN QLEERSV MEDEMNETKRGEKFREKRIKR NEQSIQEIWDYVKRPNLRLIGV LESDRENGTKLENTLQDI IQENF
27476	57844	A	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/ WLCPHLCALF*QCPP/PTCHQSA SPR\WP*G/RPAAGPHPPAATVA PKRKGKTKSSTRE
27477	57845	A	27642	237	561	

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27449	57817	A	27614	2	686	SQCAELASPLSPAPGLPRHSRL HALLGLAMPVDLSKWSGPLSL QEVDEQPQHPLHVITYAGAAVD ELGKVLTPQTQVKNRPTSISWDG LDSGKLYTLVLTDPDAPSRKDP KYREWHHFLVVMKGNNDISS GTVLSGIVG\SGPPKGTGLHRY VWLVEEQG\RPLKCDEPILASN RSGDHRGKIQRWASLPVKKIYE APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	
27451	57819	A	27616	2	346	
27452	57820	A	27617	1	305	MAISTSGSSVPWPSA/PSGPHGR GSPWGFCLATCWQSIRGQGGD PWSAGSGHPGTGASAPGPGE GQSGGDSGSA/GR*GSHLPGP ASFRAGSGQAWDGKKG
27453	57821	A	27618	287	475	
27454	57822	A	27619	37	314	
27455	57823	A	27620	1	367	
27456	57824	C	27621	360	610	
27457	57825	A	27622	604	980	
27458	57826	B	27623	8	442	
27459	57827	A	27624	1	2268	
27460	57828	A	27625	296	398	APPGPTLPWASTPSRGCT*APPG PTLPWASTPSRGCTSSWFMLPA MRRCGAPC
27461	57829	A	27626	1	3633	
27462	57830	A	27627	1853	3809	
27463	57831	A	27628	1	656	MTHNQEKKNKSTNTEMTMMM LADKDDKTAMINMLQVVKV EEAMSMRRNKDVKNHGRA RWVKPMIPALWEAKEVEGKYS AHNFWGSWKFKSSSRSSSSGPE SPARTHASFCQPDGGPTNKLGT KAFRVSPASSLLVDLNTQEVEII NVRKATPTCSLELGRKRRDGA AERAALDVVVVIYQLAPAAAP NCLNPVTSRR/PPQTPAPEGQGR RQSFE
27464	57832	A	27629	127	273	
27465	57833	A	27630	3	405	AAFHARGHRAGLSASSCSWRC CPSSAPCAPYAAPAARMLQTC LKQSPAGMPPASPSSPAHWSG STSFSKYSPRSTSTSCCPICSSCW ESWPCPTPSSPL*NKFFPASFPN RQYQLLFTQSGGENKEKDHQL
27466	57834	A	27631	689	987	
27467	57835	A	27632	228	527	

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27421	57789	A	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	A	27588	2	91	
27424	57792	A	27589	5	91	
27425	57793	A	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	A	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	A	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETHLSKLTQE\QKTK HCMFSLISGS
27431	57799	A	27596	1	1685	
27432	57800	B	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPPQKLRGRKWPVQVS\PA AGRDPGGPLL*PEGTLWGAPFC LGAPPLLTAACAPAAAGRAGGT RGAAPACPEDRTNAHSQHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	A	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKAA DKEVKKAYRQKALSCHPDKNP DNPRAAELFHQLSQALEVLTD AARAAYDKVRKAKKQAAERT QKLDEKRKKVKLDLEARERQA QGQGE*GGRRESRSTRTLEQIE RLREKGSRLQEEQRLI
27440	57808	A	27605	1	963	
27441	57809	A	27606	135	384	
27442	57810	A	27607	349	679	SETYWFFPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHQYLAQWK HRLYQRMSDLPLNDIR*FQYSK GHHRCQSNEAVQNPQQLQSL
27443	57811	A	27608	1590	2758	
27444	57812	A	27609	123	2312	
27445	57813	A	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	C	27612	77	325	
27448	57816	A	27613	1	606	

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27392	57760	A	27555	224	547	
27393	57761	B	27556	22	130	
27394	57762	A	27557	1	408	
27395	57763	A	27558	1	1011	
27396	57764	A	27559	56	822	
27397	57765	A	27560	146	411	
27398	57766	A	27561	1	885	
27399	57767	A	27562	115	1200	
27400	57768	A	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC/ H*SSGNQENELEMNKTANGDC RRDPRERSRSPIERAVAPTMSLH GSHLYTSLPSLGLAQPLALTKN SLDASRPAGLSPTL\TPGERQQN
27402	57770	A	27565	109	345	HPLFIFPDPLPPPTFHPLIGPRMC FSPGLALCPHPNLILNCSSHNSY VLWEGPGGK*FESWGRFPHDT VLVIVNKSHKI
27403	57771	C	27566	63	167	
27404	57772	A	27567	231	314	
27405	57773	C	27568	99	323	
27406	57774	A	27569	1	1347	
27407	57775	A	27570	192	269	WFKGEFLCTHS/HCLLPKRTC LLPAAM*YCDSQFSMAGETSQS WQKAKEEQRHILHGGRQKARL TWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAPPAAGVTCPFRLQP GMETPLDVLSRAASLVHADDE KREAALRGEPRMQTLPVAS\AL SSHRTGPPPIPSKRKF\SMEP\G DEDLDCDNDHVS\KMS\RI\FQPI LNKTANGRLARRDPRERSRSPI ERAVAPTMSLHGSHLYTSLPSL GL\AQPLALTKNSLDASRPAGLS PTLTPGERQQNRPSVITCASAG ARNCNLSHCPIAHSGCAAPGPA SYRRPPSATCV
27409	57777	A	27572	1	1686	
27410	57778	A	27573	1	1614	
27411	57779	B	27574	208	366	
27412	57780	A	27575	15	1729	
27413	57781	A	27578	1	1614	
27414	57782	A	27579	308	464	KAHHHWSLEKCKSEPQ*DTISW TWMKLETIILSKLPQEQKTRNC MFSLISGS
27415	57783	A	27580	291	378	
27416	57784	A	27581	2	91	
27417	57785	A	27582	439	519	
27418	57786	A	27583	2	91	
27419	57787	A	27584	2	91	
27420	57788	A	27585	2	91	



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27374	57742	A	27537	1	1590	MPNGTNESHRYNASERSQTQK DEQTGKTVGPPEWTPLVRRNG GDSGLDFHFFAEKLLIIVDSAG RAGTGHMRPPAVHFGHRGQA MITLSPLRAKQKAVLQKPPPLT STYSLMLPLFLPKRPPTTEWF LPVMEDAHELTLAWLMLALYR KPNASVQGSQAEEETLCVFRVKE PLEWQALFADVHSGVNDKGN INCSLYEHKINVSEIVLNLAQTO KNPAHSDPSSTPAGCM\PGTTA GGSVMSACCPSPAAPGPLPGP ATGSC/SPSAAPRPDPDPGGHPE GIMAIRAAPSCLGACITLQDEET CEQTHTHSRIYMIYLFARCLLH AIARGRSRKCAASAGGTCPHVR VPGGGSYFRVSLQGGQTHWMR PENGFTSCVRTKSRRCPIREQH PTKIPKALTANANQAFLLVNG HSMVASPHQSQRADLGGFWR DASSLLANSQVQVCGSLRKR HGWWVPFSLRCVAPLTADDSR LRTASLEMSTPPMHVQDDWQL RRGLPAGNTAVTVSELIYLNAN GRLQVEKFLF
27375	57743	A	27538	279	759	
27376	57744	A	27539	443	696	
27377	57745	A	27540	1	179	
27378	57746	A	27541	3	1237	
27379	57747	A	27542	4	152	
27380	57748	A	27543	760	908	
27381	57749	A	27544	203	570	
27382	57750	A	27545	312	500	
27383	57751	A	27546	1	441	
27384	57752	A	27547	1	630	
27385	57753	A	27548	1	1254	
27386	57754	C	27549	236	408	
27387	57755	C	27550	220	398	
27388	57756	C	27551	254	445	
27389	57757	A	27552	1	2742	
27390	57758	A	27553	1	744	
27391	57759	A	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN R\QINLE\LYASIVVYLSMSYVF DRD\DVALKNFAKYFLH\QSHE E\REHAECT**KL\QNQRRLAEF FLQDYQRNQD\CDDWGRAGLN \A\MECALAFWKKNVESSHYW NLHKL\ATDKN*PPIWCDFW RHIYLE*AG*KAIKRIWGDHVN QTFA/RKMGSAPNLGFGEYLF* QSTPWGSDNESSPWG

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27367	57735	A	27530	314	691	SLQGHLSDYTLTFQGCQTTQGH LPWSFTLSGKSRFSEEGTKGDV SGSQDNCGERVSRQTREQRS HRQGACYTCRKSGHWA\RNAR CPGFLSCVPSVWDPTENRTVR LTWQPLPELELWPKAL
27368	57736	A	27531	383	2907	RSPTSKTKDICHRSWRRGL/WV NKASEDGEDLDRDVSVASNIEP WTGWCRAAPLQADLGNSSSA SAPPPYNPFITSPHTWSGLQFR SVTSPPPAQQFTLKKVAGAKG IVKHALKRLKPVITRLQHG LLKPINSPYNPILPVLKPKPYKL VQDLRLINQIVLPIHPVLGII GLTSSVRRDAGQDLKRDRAE LLGDEVHHPHRRRIAEARRLL LGQHFDPLHRLIGQVLELGEA RYAPPVEQHHLAPARRTGQRL HPLEQFGQAGRAQRNRLGIE HRDRLDRPDDGAGNALAGD GDFRRGCLFAGIGIRPRYCR YRQSQDDRRPSHAAPRPRAL PIPHRPATPIADVMVMFSVA IMSQLRLVLRHIDGISRWPPA VVFITDVKIWLVPDSDCRIR SNDRDDMQGEAPAMSMNAA ARVGDPIGHSFSQGLFGEAL DGLFFARRSEVDMRAGNL GRLIARGLSGGRWTPADGQ LTLGSRDVFINGPPATMTIR STGQCRQHSGLRTVTRTETD SIGPIEVPADAYWGAQTER SLENFPFGAREQMPIGIVHA LAIVKKAARINRGHGLAGE KADAIESAAHDVIEGRHDD QFPLVIWQTGSGTQSNMNA NESSNDTFPTALHVAAAL AVTKQLFSALDRHLHAALDA KAKEWDSIVKIGRTHLQDAT PLTLGQEFSGYVQQLANARD RIEGT
27369	57737	A	27532	929	1227	PENGTFEFSILQVLDNSCHKMG KWS/RGA*RPGILLHIGPSLV SAPNVTHPKSFFFLSFLFLR SPQVPSPLNPSFLWTHLTSP LLPRLLLARLSQVPILT
27370	57738	A	27533	98	412	LGSGDLPWEINPLSSCSLLCE KHPPTTSGPQTDQPKKHLTN FKSGACYMCRK\SGHWA/RAN ARSPGFLLSRIPSVWDPT*K FGLVQLTLGKPLPELELRP RLSD
27371	57739	A	27534	14	249	
27372	57740	A	27535	49	341	
27373	57741	A	27536	392	571	

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27356	57724	A	27519	1	1618	ASSHVETRAHAEERLLKKLFSG YNKWSRPVANISDVVLVRFGLS IAQLIDVDEKNQMMTTNVWVK QEWHDYKLRWDPADYENVTSI RIPSELIWRPDIVLYNNADGDFA VTHLTKAHLFHDGRVQWTPPA IYKSSCSIDVTFFPFDQQNCTMK FGSWTYDKAKIDLNMHSRVD QLDFWESGEWVIVDAVGTYNT RKYECCEAIYPDITYAFVIRRLP LFYTINLIIPCLLISCLTVLVFYLP SECGEKITLCISVLLSLTVFLLLI TEIIPSTSLVIPLIGEYLLFTMIFV TLSIVITVFVLNVHHRSPRTHM PTWVRRVFLDIVPRLLLMKRPS VVKDNCRRLLIESMHKMASAPR FWPEPEGEPPATSGTQSLHPPSP SFCVPLDVPAEPGPSCKSPSDQL PPQQPLEAEKASHPSPGPCRPP HGTQAPGLAKARSLSVQHMS PGEAVEGGVRCRSRSIQYCVPR DDAAPE\QMARLPAPWPLATPT RLSSHPQTSPLRANAHARRSPL RCPRVPRSRPAAPKHPRTCP
27357	57725	A	27520	1	3158	
27358	57726	A	27521	2	237	
27359	57727	A	27522	76	254	PLHITFFSRACFP SLHNCCEY*Q PGF*TS\KTPQLWCQLRQYSFK HSFLVVPTCPVPLLG
27360	57728	A	27523	86	376	SLEGR LSDYTPTFQGCQT TQGR LPWSFTLSGKSRFSGEGARACY KCQKSDHQARNACSPGFLLSRI PSVRDPTGNRTVQLTWQPLPEP LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPPEPPPPGACYAC RKSGHWA\RNARSPGFLLSRVP SPPGPSRTPSFG
27362	57730	C	27525	1	381	
27363	57731	A	27526	243	437	VTSTVRQTPATSPA HKNFQMPE PQRPGVTPEPSPPGACYKCQKS DYQA\RNACSPGFLLSRVPSV
27364	57732	B	27527	88	1485	
27365	57733	A	27528	1	3759	
27366	57734	A	27529	36	438	RNDRVRPHRDVYSLQGR LSDH SPTFQGCQT TQGR LPWSFTLSG KFRFSGEGATTSPA HKNFQTPE PQWPGIPPEPPPTGACYTCRKSG HWA\RNARRPGFLLSRIPSVWD PTENRTVQLTWQPLPEPELWPKAL

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27339	57707	A	27502	1	852	
27340	57708	A	27503	3	171	
27341	57709	A	27504	1064	1302	
27342	57710	A	27505	449	668	SPGDYFISLMAAMGRPQVGYW APELLQKMMRKRMRNR/VKKLI QNYKQLK/CSLTLNNHVKLVRT NLRFHLAGLLG
27343	57711	A	27506	1	2454	
27344	57712	A	27507	2	408	
27345	57713	A	27508	205	715	
27346	57714	A	27509	1	813	
27347	57715	A	27510	1	864	
27348	57716	A	27511	17	396	
27349	57717	A	27512	3	428	LTNYAAAYCTGLLLARLLNR LGMDKIYEGQVEVPGNEYNVE SIDGQPGAFTCYLVADLARTTT GNKVFGAPEGAVDGGLSNPHS SKRFLGLSIPHSTK*ILGYDSEN KEFNAEVRKRHIMGQKFADDL HCLIEEDENASKK
27350	57718	A	27513	164	431	EFFSTSNIGVYLQIIHIVGKPI*H /YLV*ILSY*HLAARTISSKIKSN SLVPCASNRGDVGSTRPRVTR RSVRYSAAPLRSPLFAR
27351	57719	A	27514	1307	1947	TNEGSGNSAPLFGARNQTRMI VRGTNR/DIICQIAYARTEGDMI VCTAYVHELPHYGVKVDLTNY AAAYCTGLLLDRLLNRDMD KIYEGQVEATGDDYNVVSIDG QPEVHRKHIMGHNVADYMCY LMEEDEDGYKKQFSQYMKNVS TPDMMEEMCKKAHAARES CEKKPKKEVKKKKWNRPKMS LAQKKDWVAQKKASFLRAQE RAAES
27352	57720	A	27515	1	987	
27353	57721	A	27516	1521	1641	
27354	57722	A	27517	2	614	ILSRVVEFPLTAEVPPPELLAAAG FFHTGHQDKVRCFFCYGGLQS WKRGGDPWTEHAKWFPSCQFL LRSGRDFVHSVQETHSPLLGS WDPWEEPEDIAELWPPSLPLG TLSCPHPGERSSSKVPRSQEGSV QPRPRGRGGFLSPQ/DARDVEA QLRRLQEERTCKVCLDRAVSIV FVPCGHLVCAECAPGLQLCPI WQKPPSRSR
27355	57723	A	27518	3	89	

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27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCFQLLPEKKE GRLAGDAGAARPAKSGRFLGL TSGLPSEWSARTGPEPPKSLSG GGELNGSSLGFGTQDGRGTRE GRDRGLHPARPPQYQHSP
27313	57681	A	27476	541	4172	
27314	57682	A	27477	3	1110	
27315	57683	A	27478	340	1032	
27316	57684	A	27479	2	779	
27317	57685	A	27480	3	281	
27318	57686	A	27481	519	737	VPDLLLQEPNAGLCGHFCDPGD SLQCLCHQGPFGAQNWAAV WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	B	27482	1	915	
27320	57688	A	27483	68	145	
27321	57689	A	27484	1281	1433	
27322	57690	A	27485	171	708	
27323	57691	A	27486	1	270	
27324	57692	A	27487	278	588	VYIKRMPKKKV/SEGTIKEPKR RLAQLSAKPAPAKVEAKLKKA AAKDKSSGKNVQTKGKRRAK GKQAKVANQETKEDLPAENGE MKTEESPASDEAGEKETKSD
27325	57693	A	27488	304	513	PVRHGAFQDKSSDKK\VQTKG KRGAKGKQAEVAN\QETKEDL PVD\SGETKTEESPSLLIEAGEK EAKS
27326	57694	A	27489	1	435	
27327	57695	A	27490	3	273	
27328	57696	A	27491	9	293	
27329	57697	A	27492	1	504	
27330	57698	A	27493	1	529	IPPPRLFLPVATEVARVRLPPP PPQNAARDALTSYLA WASPR KQTPSPPAKDIK\KILEQRGYP KADDDR\LNKVI\SEAEWKYTL KDVIAPGVLASLPVPAAGGAV AVSACPQALAAPCCLGSAPAA AEGEEKMKKKKEEVLKES\DDD\ MGFGPFELKSLPPLQIKGLFYTS R
27331	57699	A	27494	1	396	
27332	57700	A	27495	2	398	
27333	57701	A	27496	1	702	
27334	57702	A	27497	1060	1446	
27335	57703	A	27498	46	216	HPLQLSVIPFLPVK*HVDQMGF AD/CVLSN*VNCLASRFLAVSV ALRSSRFIFTMVP
27336	57704	A	27499	1	1152	
27337	57705	A	27500	126	184	
27338	57706	A	27501	238	498	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27296	57664	A	27459	699	761	
27297	57665	A	27460	399	434	
27298	57666	A	27461	683	1661	
27299	57667	A	27462	1	95	
27300	57668	A	27463	3	517	
27301	57669	A	27464	6	401	RGLTEVPETSGGRVSVGAMAK HHPDLIFCRKQAGVAIGRLCEK CEGKCVICDSYERPCTLVRICDE RNYGSYQGRVCICGGPGVSDA YYCKEVHHPGERTRDGCASKIV NLGSSKTDLFL*TAKNTGFQER
27302	57670	A	27465	1	321	
27303	57671	A	27466	67	348	
27304	57672	A	27467	1	642	
27305	57673	B	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF PRRSYRCSHRLIICLVIGDAV* STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN QTTGKSPQLQQDYFPRRSYRCS HRLIICLVIGNAL*STVQLKAL MLRGRNYK
27308	57676	A	27471	35	3801	
27309	57677	A	27472	1	2901	
27310	57678	A	27473	1	1317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT EEVEGGIAGTDVAR/EASDFILT DAIFSSIVKAVMASLQRRGSRE L*LPAAGVWKLQTDFAQSI/AE EGIECKSIKPVLAKYLVWTRLF VGLLAELRDESAPETTPAGRRR QPQVWSGARQTCGQRTERLAG GLGEMQACSGNLGAEKEKQSK KLAGGWPMSPSTLHALGPKLV PAKSQRHRAEHMSTWQVGVVS SSYFTGNLVGTLTGYVIKRGF NRSYYLASFIFAAGCAGLGLMI GFWSWLA WRFVAGVGCAMIW VVESALMCSGTSRNRGRLLA AYMMVYYVGTFLGQLLVSKVS TELMSVLPWVTGLTLAIGLPLL FTRVLNQQAENHDSTSITSMK LRQARLGVNGCIISGIVLGSLYG LMPLYLNYKGGKSSPTPAVRPA RHNSLPGPEAKKYRPGFIHGLTS CIAFSVQAANVDEYITQLPAGA NLALMVQKVGASAPADYHSQ QMALPASTQKVITALAALIQLG PDRFTTTTLETGKNGVENVLKG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27270	57638	A	27433	93	866	TVSFPATGC\QKLIIE\DDERKL RTFYEKRMATEVA\ADALGEE WKGYYVVRISGGNDKQGFPMK QGVLTG\RVRLLLASKGHSCY RPRRT\GERK\RKSSSVGCI\VDS KSWSVLQLGLLLKKKKK*RRIF PG\LTDTTVPRRLGPQK/RASRIR KLFNLSK\EDDVRQYVVRKPLN KEGKKPRTKAPKIQRLVTPRVL QHKRRRIALKKQRTKKNKEEA AEYAKLLAKRMKEAKEKRQE QIAKRRRLSSL\RASTKSSESSQ
27271	57639	A	27434	2	401	
27272	57640	A	27435	1373	1838	
27273	57641	A	27436	1	257	MNRQLSDSYTEDTKEPSDVTTT ERTRSPPGSAKTTMIDTLKKLQ DV\QKLRTPKIPQSQQQICWNN MSRLRDQS*RSSKKRQRLWK
27274	57642	A	27437	247	831	
27275	57643	A	27438	1	993	
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE* RPFQP
27277	57645	A	27440	274	482	
27278	57646	A	27441	1	219	
27279	57647	A	27442	1	681	
27280	57648	A	27443	11	1094	
27281	57649	A	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS PN*LGLPIPLSMVLCEIIHF
27282	57650	A	27445	1	1563	
27283	57651	A	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	A	27448	7	259	
27286	57654	A	27449	29	191	
27287	57655	A	27450	2	519	KSQDYKSLNATCAGGTSFSGC ARRLLLSTCSSGWRSGLSLRG GKMELEA\MSRYTQPSEPQLSS PHLTVVLLAIGMFFTA\WFFVY EVTSTKY\TRDIYKEAPHP*YA LTPSMGFGVLF\LLL\WVGIRV SHPRVTTQNGFHWKPAFCKINF FFYLFAWEVFPPAAHNKVQML
27288	57656	A	27451	144	386	VCECKMPKVQPNFTHWSRS*N DDLNRSSLWQA*PQAASVEIIIL RS
27289	57657	A	27452	462	672	
27290	57658	A	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	A	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	
27295	57663	A	27458	2852	2935	

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27253	57621	A	27416	2	670	IAGEITRRGSRARPRPGPQC PPGTAMIKAILIFNNHGKPRLSK FYQPYSED TQQIIRETFHLVSK RDENVCN FLEGGLLIGGSDNK\
27254	57622	A	27417	5	379	LIYRHYATLYFVFCVDSSESEL GILDLIQVFVETLDKCFENVCEL DLIFHVDKVHNILAEMVMGGM VLETNMNEIVTQIDAQNKLEKS EAGLAGAPA\RAVSAVKNMNL P\EIPRNINIG\DISIK\VPNLPSFK
27255	57623	A	27418	536	675	LEWSSAKFPTAVGVSLLLSSVC RSQ*FLMDAMSRMDLVRYTSA RVS
27256	57624	A	27419	2	1220	
27257	57625	A	27420	435	552	
27258	57626	A	27421	5	379	
27259	57627	A	27422	1	1062	
27260	57628	A	27423	17	467	
27261	57629	A	27424	105	355	
27262	57630	A	27425	283	466	APRSARPIVHG VKATRPKPRNL LDKDMFSKSDPLCVMYTQGM NKQWR\IEFGRTEVIDNTLN
27263	57631	C	27426	167	379	
27264	57632	A	27427	164	1185	
27265	57633	A	27428	1	873	
27266	57634	B	27429	20	523	
27267	57635	A	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLFLRILPL FADKVPKTAENFRALSTGEKGF GL*GVPCFHRIIPGFM\CQGVGDF T\RH\NGTGGKSIYGEK\FEDENF ILKHTGPGILSMANAGP\NTNG SQFFICTAKT\EWLDGKPVVFG KVKE\GMNIVEAMERFGS\RN KT\SKKITIADCGQLRIKFDLVF YSLTTKIIPSGSPRESTPPTHLLA SILES\CSRLQFPFGFHVFLVPS
27269	57637	A	27432	27	410	LQDEATGCQKLI EVDDERKLRT FYEKRMATEVAADALGEEWK GYVVRISGGNDKQGFPMKQGV LTHGRVRLLLSKGHSCYRPRRT GERKRKS\RGCIVDAN\SVLN LVIVKKGEKDIPGLTDTTVPR



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27243	57611	A	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ SPADLEEKKEEDSNMMKREQPR ERPRAW\YPHGLVGLHNIWT DLACLNSLIQVFVMNVDFTRIL KRITVPRGADEQRRSVPF\QML LLEKMQDSRQKAVRPLELAY CLQKCNVPLFVQHDAQAQLYLK LWNLIKDQITDVHLVERLQALY TIRVKDSLICVDCAMESSRNSS MLTLPLSLFDVDSKPLKTL\EDG LHCFFQPRELSSKSKFCENC KKTRGKQVLKLTHTLPQTLTIHL MRFSIRNSQTEKDLATPLYFPQS LDFKPRSFQKRESCDAEEQS GGQYELFAVIAHVGMADSGHY \CVYIRNAVDGKWFCFNDSNIC LVSWEIQCTYGNPNYHWQET AYLLVYMKIMEC
27244	57612	A	27407	1	1077	
27245	57613	A	27408	3	242	
27246	57614	A	27409	213	928	EGPARQRLSPVRASKMTKKR RNNGRAQKRAAAHVRGPSPLK/ CFPSGPLPPNCAR\CVPQGTRPI KKF\VIR\NIVGGRSRQGHISEAS RLRMPISLPKL\YVKLHYC\VSC AIHKQK*FR\NRS\RESPAKTRTP PPRF*DLAGGCPTVPPPKAHDL GPEYCRHQTCVNWVCCRQATI LGKELCGQIRKLPSQQMSPGWL PSGYSCWLYKYKTEATTALQS RGEVYHPLQALWSRPPGRDPL
27247	57615	A	27410	1	267	
27248	57616	A	27411	257	322	
27249	57617	A	27412	2	176	
27250	57618	A	27413	218	923	
27251	57619	A	27414	2	429	TKFAARRPALAACA AISKIKAR DLRGKKKEELLKQLDDLK\VE LSQLRVA*VTGGAASKLSKIRV VRKSIARVLTINQTSKGKKTFR EILTRGKKYKPLGPCGP*GRTR AMRRRLNKHEENLTKKKQQRK ERLYPLRKYAVKA
27252	57620	A	27415	1	1146	

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27235	57603	A	27398	1	490	
27236	57604	A	27399	150	536	NCKISFLHFCYIFVKALKKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRA L*G*DLTHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
27237	57605	A	27400	336	928	
27238	57606	A	27401	13	724	INPPPPFRPEPPSSSKFAKNDGP QRGKRRGTPIIMFS/RGPFKKT GVVPLAHIFMRVYKQRCDFVDI QGEWGTLFQKGNCPHKVVTHG QNLEGVLPMTVPAVLVGHLL* NKQV*GQRFLPKRNLMWRI*A HLRHF*GARD/RASLKTGREN GSRKKERKPKGGKVTWGFQLK RRHLGFPPQEEATFLLKEPIGGR EP*ACLEPYFPYWISWGINRVF KKKIKGPSGLQKKKKKKVD
27239	57607	A	27402	1	759	
27240	57608	B	27403	1	372	
27241	57609	A	27404	1746	2966	DMKNGAKEGESYLLQLCPSP LPSPSPSPSPSPSPSPSPSPSP SPSPSPSPSPSPSPSPSPSP SPSPSPSPSPSPSPSPSPSP PSPSLPPLPSPSLPPSPSPSPSP PSPSPSPSPSPSPSPSPSPSP PPSPSPSPSPSLPPSPSPSPSP PSPSPSPSPSPSLPPSPSPSPSP HHHHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHHHHH HHRHCHHHRHHRQHRRHHHH HHHHHHQHHPQTLH*PSESQ HIVGAQ*MLHCHSLCVYIQGSH SVRKFLVLKQKLSMGMVLPPG GDLEHCGACLDQDQDWRACAM PSHKYPPKHAHCCGCLC
27242	57610	A	27405	150	462	ICEGRTCIFEEPCNCSSLYVRN GGNHSHTTTFKYNGSNWIPR WQGPGSGTQPSKARRPVAFSQG NCAMEKGN*SDILGTTEHWL*A DIDSRGPKMSLQSSS

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27212	57580	A	27375	1	2355	
27213	57581	A	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV EMQGDDEMTRJIWELIKEKLIFPY VELDLHSYDLGIENRDATNDQ VTKDAAEAIAKKHNVGVKCATI TPDEKRVEEFKLKQMWKSPNG TIRNILGGTVFREAIIICKNIPRLV SGWVKPIIIGRHAYGDQYRATD FVVPGPVKVEITYTPSDGTQKV TYLVHNFEEGGGVAMGMYNQ DKSIEDFAHSSFQMA\LSKGWPL YLSTKNTILKKYDGRFKDIFQE MYDKQYKSQFEAQKIWYEHR L\ID\DMVAQAMKSEGGFIWAC KNYDGDVQSDSVAQGYGSLG MMTSVLVCPDGKTVEA\EAH GTVTRHYRMYQKQGQDVHPI LASIFAWGPEGL\AHRAKLDNN KELAFFANALEESFYETHE\AGF MTKDLAACIKGLPNVQRSDYL NTFEFMDKLGENLKIKLAQAK
27214	57582	A	27377	1	692	
27215	57583	A	27378	251	2150	
27216	57584	C	27379	93	293	
27217	57585	A	27380	308	534	
27218	57586	A	27381	2	856	
27219	57587	A	27382	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCGVEALTTLEVAGRM LGGVAKQEKKKKKTGRAKRRM QYNRRFVNVPVPTFGKKKGPN
27220	57588	A	27383	150	456	
27221	57589	A	27384	651	835	
27222	57590	B	27385	1	2193	
27223	57591	B	27386	109	714	
27224	57592	A	27387	150	458	
27225	57593	A	27388	1	2055	
27226	57594	A	27389	1	804	
27227	57595	A	27390	645	1828	
27228	57596	A	27391	899	1216	
27229	57597	A	27392	79	156	
27230	57598	A	27393	1796	2215	
27231	57599	A	27394	107	724	
27232	57600	A	27395	854	926	PLEIPHEPPPGRG*HAPQLPRGQ
27233	57601	A	27396	2	413	
27234	57602	A	27397	54	442	FAKMTNTNLNRRGTRYMFSSRP FRKHGVVPLATYMRIYKKGDI VHIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVNKQG KGKILAKRINVRIEHITHSKSRH SFLKRAKENDPEYEEALENGT

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27199	57567	A	27362	552	2325	
27200	57568	A	27363	693	1270	
27201	57569	A	27364	18	146	
27202	57570	A	27365	270	683	
27203	57571	A	27366	1	1398	
27204	57572	B	27367	1	1152	
27205	57573	A	27368	40	538	SPSPKDS PGVRVGISCYIGGPCQ QRLSPVRASKMTKKRRNNGR A\KKGPRHVRGPSPLKFLPPSSC HLTVPRCRAQGT RPICKFVISK P*VEAAA\VRDISEASVFDAYL\ LPKLYVKLHYCVSCAIHKQK*S GNRS\REA\RKTRTPPPRFR\PGG *LPHGPPTKSP
27206	57574	A	27369	204	401	
27207	57575	A	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	A	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWMLGSL LARAQVRASAPRHLFSRSLRRG LSFSDTEARCARELIHVHTSTN APARTEAYPAGSAEPPRRPRAG REHSFFSQRYVPLPPLGGALGS GPAKLPPRAPCPVRF CADLET LCGALDCYKVRGGAAPARPAP RPAGGIQVSSLSGFGTESLPGGN PFPHRDHRESGTMDSPSLTVAT PLSLTPPIPRELACGDWRRVGG GAGGGGLRRRGLGGDKAGKR KSSDLPCGPGFLQSLQKRRHW ESGLGLPGCGCESELVSGCGAP TLRQHII PAEGRNGVKEKSADL GCGGSQGLRAKKG TNPGIENG KRKGKEGMLDAWICRRSAFGP GREKLGGEVGCNDKGKIRFIE VKMSKKISGGSV VEMQGD EMT RIIWELIKEKLIFPYVELDLHSY DLGIENRD/ATNDQVTKDAAEA DKKHNV\GVKCATITPDEKRVE EFKLKQMWKSPNGTIRNILGGT VFREAIICKNIPRLVSGWVKPIII GRHAYGDQGFSGNMQNAIMK KLKWLHLARVGKFS DANAKFY CRLYYAGEFHKMREVILDSSEE DFIRSLSHSPWQARGGKSGAA FYATEDDRFILKQMPRLEVQSF LDFAPHYFNYITNAVQQRPTA LAKILGVYRIGYKNSQN NTEKK LDLLVMENLFYGRKMAQVFDL KGLRNRNVKTD TGKESCDVV
27211	57579	A	27374	2	2138	

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27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSQ GRYCSSFNRVVRQNSSDAKVV NVPKTRITFCKK\CGKHQPHKV TQYKKGKDSL\YAQGRRRYDRK QSGYGGQTKPIFRKKA\TTKKI VLRLECVEPNCRSKRMLAIKRC KHFELGGDKKRKGQVIQF
27179	57547	A	27342	1	565	
27180	57548	A	27343	1	1050	
27181	57549	B	27344	1	2109	
27182	57550	A	27345	2916	3229	
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL W/RKKPSDVHAFFLR\VRGQT RSFFVFTGVPRPTRPKARRLG YKAKQGYVIYRIRVRRGGRKRP VPKGATYGKPVHHG\NPA*KF ASKALQVPLPEGTEAGR\HCGG S*ESLNSYWVGEDS\TYKFFEVI LIDP/YSHKAIRRN\PD\Q\WIT\K PVH\KHREMRGLTSAGR\KSRGL GKG\HKFHHTIGGSRRAAWRRR NTLQLHRYR
27184	57552	A	27347	1	1646	
27185	57553	A	27348	2	2600	
27186	57554	A	27349	1	2403	
27187	57555	A	27350	100	520	
27188	57556	A	27351	1	570	
27189	57557	B	27352	1	837	
27190	57558	B	27353	1	1434	
27191	57559	A	27354	1	2379	
27192	57560	A	27355	3	952	IDWAPKSDRIVTCGADRNAYV WSQKDG\VKPTLVILRINRAA TFVKWSPLENKFAVGSGARLIS VCYFESENDWWVSKHIKKPIRS TVLSLDWHPNNVLLAAGSCDF KCRVFSAYIKEVDEKPASTPWG SKMPFGQLMSEFGGSGTGGWV HGVSFSASGSRLAWVSHDSTVS VA\DASKS\VQVSTLKTEFLPLL SVSFVSENSVVAAGHDCCPMLF NYDDRGCLTFVSKLDIPKQSIQ RNMSA/LWERFR\NMDKRATTE DRNTALET\HQNSITQVSIYEV D\KQDCRK\CTTG\NDGAMTIW DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	A	27359	425	667	
27197	57565	A	27360	121	401	
27198	57566	A	27361	1	1818	

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27163	57531	A	27326	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRAILYKRLKVPPAINQFTQAL DRQTATQLLKLAKHYRPETKQ EKKQRLARAEEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVDPIELVVFLPA L\CRKMGVPYCIKKGKARLGR L VHRKTCTTVAFTQVNSEDKGA EAKLVEAIRTNYNDRYDEIRRH WGGNVLGPKSVARIAKLEKAK AKELATKLG
27164	57532	A	27327	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSES RHQISCMCAA STWMERTAYGGSHRELLQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI
27165	57533	A	27328	908	1331	GDMRGRREGGFGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLT MPLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPEKRDPL RVKDQGRHPCVV
27166	57534	A	27329	1	1134	
27167	57535	A	27330	62	310	
27168	57536	A	27331	243	578	
27169	57537	A	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL LLFAP*ERSTYDLRSSDRPAQET SHQFQIRERQRRHVLSVDPKLR RRSRTGKAAPWCLIIAGTPL*L YTHVSRVSDHAGMPALVLHP* R/LSPFTLGKGQHALKGLKPVIT RLLQHGLLKPINSPFPSPILPVLK PDKAYKLVQNLRLINQIVLPIHP VVPNPYTLSSIPPSTTHYSVLD LKHAFFTIPLHPSSQPLFAFT
27170	57538	A	27333	1	1860	
27171	57539	A	27334	1	957	
27172	57540	A	27335	97	826	
27173	57541	A	27336	245	392	
27174	57542	A	27337	736	1300	
27175	57543	A	27338	590	891	
27176	57544	A	27339	1256	1654	VQPVRLVSGMQHPGSGWRRL WGQHSTSLTSKEHLHISKRGNI DNLVQRNMPSPNEKPKCELP FPSCSTVHFIIFFVVVQTVLFIGY IMYRSQQEAAAKILLTTIFLCT SSICVQNDVVLREFKYLNCFIV
27177	57545	A	27340	295	852	

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27153	57521	A	27316	63	641	FAKMTDHHKGERGEATRYMFSR PFKKTMGVVPCGHNN*RFYK\K GDIVDIKGMGYCVQNGMP\HK CYHVGKTGRSLTIVTPACLLPLL *TNQF*GKVFS\KRINVRIEHIKH \SKSRDSFLKRVKENDQKKKEA QEEGTWVQLKRQPAPPREAHF V\RTNGKEPELLEPIPYEFHGIN RCPKKKIKDLWATKKKKK
27154	57522	A	27317	1	390	
27155	57523	A	27318	75	394	IWGDVEKGKK\IFIMECSQCHT VEKGGKHKTGPNLHGLFGRKT GQAPWDTPTYAANKNGHIIWG EDTLMEYLENPKK\YIP\GTKMI FAGIKKKEERADLIAYLKKS
27156	57524	A	27319	2	529	ERQTRHAGGVRRGPRPKLQRD KAAAAAVLGAVRKRPSVVP AGQDPALSTSHPFYDVARHGIL QVAGDDRFGRRVVTFSCCRMP PSHELDHQR\LLEYLKYTLQY VENDYTIVYFHYGLNSRNKPS LGWLQSAYPEFDRKYKKNLKA LYVVHPTSFIVLWNILKPLISH KFGKK
27157	57525	A	27320	287	445	
27158	57526	A	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKQRLARAEEK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQL\CRKMGVP YCIKKGKARLGRLVHRKTCTTV AFTQVN
27160	57528	A	27323	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLARAEEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLLVIAHDVDPIELV VFLPALCRKMGVPYCIKKGKAR LGRLVHRKTCTTVFT
27161	57529	C	27324	62	217	
27162	57530	A	27325	1	1545	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27141	57509	A	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIGLFAADKGPRTA*FSCL* SIEEKGFGL*GVPCFHRJIPGFM\ CQG\GDFTRH\NGT\GGKSHPM GKKFE\DENFILKHTG\PG\ILSH GKCLDPNTNGSQFFICTA\KTEV VGMAKHVVFWQK*KKGMKYC GRPWERFG\SR\NGKTQQRKITI C*LVGQLRNKVLTWWF
27142	57510	A	27305	72	387	VCLQHGPWSSLKHVQGWRRD CHGLSLGPRTHVQAGTLPKPTL WAEPGSVITQGS\VTLWCQGI LQTQEYRLYREKKTAPWITRIP QEIVKKGHDPIPSITWEHTG
27143	57511	A	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	A	27308	1	1419	
27146	57514	A	27309	198	1634	
27147	57515	A	27310	78	216	
27148	57516	A	27311	1	489	
27149	57517	A	27312	18	463	AEGVEPGSPRVVLESEQFLTE LTRLFQKCRTSQSVYITLKKYD GRTKPIPKKGTVEGFEPADNKC LLRATDGKKKISTVVSSKEVN* VFRWLISNLP\GANMDGLKKR DKKNKTKKTKAAAAAAGP AAAATAATTAATTAATAAQ
27150	57518	A	27313	1	1242	
27151	57519	A	27314	147	965	DPPSPVPAPPSSPRDGHFLVPDA TMAEEQPQVELFVKAGSDGAK IGNCPFSQRLFMVLWLKGVTFN VTTVDTKRRTETVQKLCPPGEL PFLLYGTEVHTDTNKIEEFLEA VLCPPRYPKLAALNPESNTAGL DIFAKFSAYIKNSNP\ALN\DNLE EGTPGKP*RFLDNYLTSP\PEEV DETSAEDERCLSDGTFLDGNEL TLADCNLLPK\HIVQVVCKKY RGFHHPRPFRGVAFGYL\SN\ YARENFRFPVPDDEEIELAYE QVAKALK
27152	57520	A	27315	1	933	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27128	57496	A	27291	304	642	
27129	57497	A	27292	75	393	
27130	57498	A	27293	1	678	VFGLGSAHMLLNKTFGSYLGVNLGFGFGVTMGVHMAGRSGAHMNAAVSLTNCALGRVPWRKFPVYVLGQFLGSFLAAATISLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRWHHLPLGLHWHHPTGAPEIGGFCGV
27131	57499	A	27294	2	1694	
27132	57500	A	27295	1	356	GIFVTYLPDHMTLWRGFLNEAWLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWGKQVFRYFPCPGPIPLSFSVGPLCVEGWGVM
27133	57501	A	27296	1	544	
27134	57502	A	27297	320	610	LREYINIHTAHPMEWASKKRAPRALKEIRKFAMKEMGTPDVRI DTRLNKAVWAKGIRNVPYRIRVRLSRKARNEDESPNKLYTLV TYVPVYHFQK
27135	57503	A	27298	1	303	
27136	57504	A	27299	1	1311	
27137	57505	A	27300	1	3126	
27138	57506	A	27301	2	779	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKGPRGTA*FSLL* ATGEKGFGL*GVPCFHRIPGFM \CQG\GDFTRH\NGT\GGKSHLW GRNLKDENFILKHTGPGILSHG KMLDPNTNGSQFFICTAKT\EW LDGK\HVVFVKV\KERHEILWEA MGALLGPRNGKTQQEEPIVPG GQLRIKFDLVFYSLTTKIIIPFCSF KESTPPPHLLASILESLCSRLQFP FGFHVFLVPCA
27139	57507	A	27302	143	390	
27140	57508	A	27303	249	1516	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27107	57475	A	27270	147	224	RLTLPDHLGSLLDHHR\ALGNS YSGG
27108	57476	A	27271	1	837	
27109	57477	B	27272	184	288	
27110	57478	A	27273	1	286	
27111	57479	A	27274	1	699	
27112	57480	A	27275	1	3660	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRV DGQKQV KLSVLQEKS AQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPVPFRSQEVV ETMCPVPAAATSNVHVMVKKISI TERSCDGAEMKWEDQNIGD
27113	57481	A	27276	1059	1229	
27114	57482	A	27277	2	4735	
27115	57483	A	27278	415	825	SCADFQDYWDQREYTYNRPHT ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFLCISLSF GSHWGSVPGNWWLTYSWG/SL VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMGLDNSL EQIN
27116	57484	A	27279	1	1326	
27117	57485	A	27280	2976	3068	VWTALTNR LGQQVSICG*PGTE DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHGRLRWV ITHIRLVISWATYLVQNNIIQTR LF
27119	57487	A	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	A	27284	1	4560	
27122	57490	A	27285	87	237	LLFFQLGGDAFSFKFSSGVNFR NSLICQAWGKRVFSALLCILSE YTSPL
27123	57491	A	27286	1	246	
27124	57492	A	27287	46	396	
27125	57493	A	27288	1	552	
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSESGSGPPARIVKMSLR KQTP/SDFLKQIIGRPVVVKLNS GVDYRGLVLA CLDGYMNIALE QTEEYVNGQLKNKYGD AFNR GNNVLYISTQKRPDVRTPKRA TLFIVGYIFL
27127	57495	A	27290	202	450	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27087	57455	A	27250	2	235	
27088	57456	A	27251	3	1393	
27089	57457	A	27252	28	271	
27090	57458	A	27253	12	485	RMAFCRASQADQDRFICIYPAY LNNKKTIAEGRRIPISKA VENPT ATEIQDVCSAVGL\NVILRKIKM YF*EWN RDVQYR\GRVRVQLK QEDGSLCLVQFPS/RLYTKPNF WFLGKSVMLYAAEMIPKLKTR TQKTGGADQVFQQGEGS*KGK GKQKEVT
27091	57459	A	27254	1689	2176	APPGMGAASLCAFGLLVTFAT ASPRYAMVQPSFRLGTLKGQA EADFPFVSSGVSPPSFLSPLLPA APGARRG*LQRGDLGRQAPPPA PGCAPGLA*GRPPAPHL*RLCSR PTFFPPPANSSRLALADSPPPRQ LQGARP*PVPGRLLTSTGTTPRPL PRPLGP
27092	57460	A	27255	263	439	
27093	57461	A	27256	1	499	MSELPTIATKRIKHLGIQLTRD VKDLFKKNYKPLFNEIKDDTNK WKNIPCLWIGRINILKMAILPKV IYRFNAIPIKLLMTFFTEMENTT FKFMWNQKR/CPHCQDNPKPK EQSWRHHAT*LQTI LQGYSNQN SMG/TWMKLETIILSKLSQGQK TKHRMFSLIGGN
27094	57462	A	27257	1940	2062	
27095	57463	A	27258	1232	1432	
27096	57464	A	27259	168	1189	
27097	57465	A	27260	1	1760	
27098	57466	A	27261	453	543	
27099	57467	A	27262	873	962	
27100	57468	A	27263	8	411	FSRCRCSGR/YLCMASCL\CFHH CWWMA SHHWPI*RTQV*CAC WEGRHLG\CA PKCLSLLGFTRL LACVLWLPILQSVIPIHIQVSITV RVLF AAAHDEARASEATFQESG GPYPLLSTPLILLKAVVVLMLD AHAS
27101	57469	A	27264	1	552	
27102	57470	A	27265	828	1211	
27103	57471	A	27266	428	655	DQKVPPLEMYFGIEVKS LKQLR SISA*SLFSSRALKEDSGLLKLK QPRSSGVIPRRFIVSWPWKMVR QPVLFSVG
27104	57472	A	27267	1	855	
27105	57473	A	27268	1	1261	
27106	57474	A	27269	164	260	

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27070	57438	A	27233	3	1107	AVFLSFGWWPLPGIGFQSAEGE AAWTAAPAPSAPPPSKPRARPP RPEPAASYLSALPPPPRPSERPS MQAIKCVVVGDAVG\KTCLL ISYTTQCHFLGEYIPTVFDNYS A\NVMDGKTGEIWGLWDTAG QEDYD\RLRPLASYPANRMCS*I CFS\LVSPA\SFENV/LVQKWYPE VR\HHCPNTPNIPVGT\KLDLRD DKRHDSRNLKEKKLT\PIITYPA GS*AMAK\ERLGAVKYLGCAP AAHTSEGLKTVFDEAIRA\VLCP PPVKERGRENCPLVVNVSAPSF LGSCPLGTFCRLCSKKNKKKKQ KKKNNGGAFALNANFLLQINF IKPFFEPISNFKVLFVLNVRVQT HILLKFSPKMTSLLKALFFK
27071	57439	A	27234	3	203	
27072	57440	A	27235	1	112	LGNTWG*QPCKRLKIWLSLEFT KINVIRHMWKKFKRL
27073	57441	A	27236	1	513	QHWGRYLKRAFEQWQVPRFG HMPDPGPVKPLQPVEVETRG DYKLLFHFWDEWLKFSAD FFIPGKLCAIVF*KRL*RP GAVAYACNPSTLGSRG RWIT*GQEFETSLTNKE VKVLSIDQRNFKLRSI GWGEFSLSKHPQGTEV KAITYSAMQVYNEENPE VFVIIDI
27074	57442	B	27237	125	302	
27075	57443	A	27238	93	432	
27076	57444	A	27239	3	279	
27077	57445	A	27240	263	446	
27078	57446	A	27241	237	369	
27079	57447	A	27242	389	836	
27080	57448	A	27243	1422	1580	
27081	57449	A	27244	103	444	RSLTCPGDMFPVVLVNIQ LLLTIANFCSWLES LPRKWDFLFYCI VRLQIFQTFMLC FLLNTLPLRNF FYQIP*IISLKFK VPQISKA EAKCHQSLCIG RVTFTPVPNK FFISI
27082	57450	A	27245	3	242	MHRNAQHHVKTA KPWGLHPL KPQPK*YSGPF* PPLEQLRCKAT GP*GCTQGGG PGPGQNNFSL LLGLQACDGRD CHEGL
27083	57451	A	27246	506	664	
27084	57452	A	27247	1	1515	
27085	57453	A	27248	269	541	RFPNLNS*LLYTR GLTPHESCQ GLGLAPSEAMA QTIPWPLLATA RLAVTGNQIL MQISAAGLN FSSENGAFISIA LSGCKFFKLL CSAS
27086	57454	A	27249	1	564	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27056	57424	A	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ PPSSMCVSAADLWLC\EAGKLL VVPMDGSHWFTMRSVVEKLIL RGHEVVVVMPEVSWQLGRSLN CTVKTYSTSYTLEDLDREFKAF AHAQWKAQVRSFLSFLSSNG FFNLFFSHCRSLFNDRLVEYL KESSFDAVFLDPFDACALIVAK YFSLPSVVFARGIGCHYLEEGA QCPAPLSYVPRILLGFSDAMTF KERVNRNHIMHLEHLFCQYFSK NALEIASEILQTPVTAYDLYSHT SIWLLRTDFVLDYPKPVMNMI FIGGINCHQGKPLPMEFEAYINA SGEHGIVVFSLGSMVSEIPEKKA MAIADALGKIPQTVLWRYTGT RPSNLANNTILVKWLPQNDLLG HPMTRAFITHAGSHGVYESICN GVPMVMMPLFGDQMDNAKR METKGAGVTNLVLEMTSEDLE NALKAVINDKSYKENIMRLSSL HKDRPVEPLDLAVFWVEFVMR HKGAPHLRPAAHDLTWYQYHS LDVIGFLLAVVLTVAFITFKCCA YGYRKCLGKKGRVKKAHKSK
27057	57425	A	27220	1	2022	
27058	57426	A	27221	124	205	
27059	57427	A	27222	248	443	
27060	57428	A	27223	263	415	
27061	57429	C	27224	1	717	
27062	57430	A	27225	349	1125	
27063	57431	A	27226	629	796	
27064	57432	B	27227	1	388	
27065	57433	A	27228	2	346	
27066	57434	A	27229	448	555	
27067	57435	A	27230	2	423	CEPIKVYVVGN\GAVGKTCLLI SYTTNAFPGEYIPTVFDNYSAN VMVDGKPVNLGLWDTAGQED YDRLRPLSYPQTDVFLICFSLVS PASFENV/LCKGAVKYLECSAL TQRGLKTVFDEAIRAVLCPPPV KKRKRKCLLL
27068	57436	A	27231	1	1503	
27069	57437	A	27232	1	635	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27042	57410	A	27205	230	2579	
27043	57411	A	27206	1	2433	
27044	57412	A	27207	1	528	NHQIRNDFTISPGVKADSRTSPI PQQPASSFDITEAAVSFAKDSL GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP TQALNFTFKDKYKQIFLDGV RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADV GKAGAERELRGFGDCLVKIYKSDG IK
27045	57413	A	27208	1	292	MTSKDKTSRGITRQQHSR FKKIRCSAATTAGTQANRV WSGPLANSNRPAAEAGVST AAAPDGPPPSVPTVDS DSLESQFKCDNLKTCH TSHGSMVMAETAVINHK KRKNSPRIVQSNDLTEAA YSLSRDQKRMLYLFVDQ IRKSDGTLQEHGICEI HVAKYAEIFGLTSAEA SKDIRQALKSFAGKEV VFYRPEEDAGDEKGYE SFPWFIKRAHSPSRGL YSVHINPYLIPFFIGL* PDKEGNEIWVDMYTVK PSGWTVRTFDKPRKR FIAFFIAGILFRAIKNH FLPRETLQCLPYILT GFRRGQSEYFSIFSN MDLADTVMFL
27046	57414	A	27209	1	1452	
27047	57415	B	27210	53	844	
27048	57416	A	27211	281	624	ACSDVWSKFRLRWSPN PRCQERPSAEKMSPHPP SAARHQASWSARRLTQ WPRPCHTQ*GQSEEH GHRSGLMPAGVTHQLP DEHAITPHLQSTAPII PEPKTLSHKDSSLQGT GK
27049	57417	A	27212	3	411	
27050	57418	A	27213	265	480	LDTILTASDGRPTYTP P*FLLLS/CFCYGF FCYIFGCSCRALARAR AGGGGVPAAHRAAGR GSRAPERIPPH
27051	57419	A	27214	294	620	
27052	57420	A	27215	1	420	
27053	57421	A	27216	1	342	
27054	57422	A	27217	175	244	DLLEMGSSFFVQCRT AIL*RKQN
27055	57423	A	27218	11	951	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27016	57384	A	27179	1	812	MPTVLACPAFDSRGSPICRFDPPELTSGVRALEESPNAITLPVCGRDVKFTLEVLRGDSVEKTSRVWSGNERDQELLTEDALDDLIPSFLTGGQTPAFGRRVSGVIEIADGSRRRKAALTESDYRVLVGELDDEQMAALSRLGNDYRPTSAYERGQRYASRLQNEFAGNISALADAENISRKIITRCINTAKLPKSVVALFSPGELSARSGDALQKAFTDKEELLKQQASNLHEQKKAGKRSRRLHHTLLRVVAEIDKPDP RDELAGLLQFAGGPLQTLFAWVSPVEAAEQRLLLAPSSGSFIP EG*DHPVRPQ*AAPGHVHYLTI PERSSQHYHPGALQE
27017	57385	A	27180	306	701	
27018	57386	A	27181	1	396	
27019	57387	A	27182	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	B	27185	23	268	
27023	57391	A	27186	1	363	
27024	57392	A	27187	2	398	TKFAARRPALAACAAISKIKARDLRGKKKEELALKQLDDLKVELSQLRVAKV/TQGAASKLSKIRVVRKSIARVLTVINQTSKGKTFREILTRGKKYKPLGPCGP*GRT RAMRRRFKPGSTEGEP*RTQGSR
27025	57393	A	27188	224	547	
27026	57394	A	27189	1	888	
27027	57395	A	27190	280	1170	
27028	57396	A	27191	1	191	
27029	57397	A	27192	438	1240	
27030	57398	A	27193	168	378	
27031	57399	A	27194	1	1362	
27032	57400	A	27195	2	918	
27033	57401	A	27196	38	397	RRCRPTMPRP\WCTCRGYQGPRKAQGG*AQDPKGCQPQARSTCLHCPPQAWR/VLVPVLPVLRGSGCAGQ/MAKAKAKAKDQTKAQAAAPASVPAQAPKRTQAPTKASE*ISLPT*GQKDWCDP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	C	27200	164	274	
27038	57406	A	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	A	27203	164	409	
27041	57409	A	27204	152	380	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27002	57370	A	27159	1	519	GQLI/LKDTFITQSAADIRRKFO KQALGPEHNLEALLNLAILVYF NRDQEEQAQKEKRDQRKAAPL IMALRQTLVVQRGQKMEQANH LIPGYSEIARPLYTLIKEIQRANT HQVEWEPEAETAFKPLKQALV QAPALSLPTGQNFSLYITERAGI ALGVLTQTHGTTPLVAYL
27003	57371	A	27160	72	381	DSHTRSGTTRWGIRCSGSSPSR RARWGRWGGLAAVALRRPAP AAGGTA <del>PRGCL</del> PAA*GSPPAPP SGS*SGSSDRPARMPLVVGLSH EFE*GLAGVDGEVLPPSRCVAL LLLRVERLHVAVYLPREALHQL HPLALDLLIARLVCHWLWG CPTSLSKDSKSYSCSLCDV
27004	57372	A	27161	515	747	SHGNSGNFQGTTRDTISLS*AQLT TSTKDPWTDPPALWPRVFPSGG HYNCRAPSSP/TIQQEVARAVIT QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	A	27165	1	691	
27009	57377	C	27166	1	1491	
27010	57378	A	27167	830	2592	
27011	57379	A	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH RSPRSGGGSGARRAAGPKPCSP RSDAPAQPRGRSRRVLPLQVQ AEPPEPWPVLPAAKPLARPEA GMAGPGGRRTTSLPRRRGCGC CCPASSCFSSLSC
27013	57381	B	27176	1	1392	
27014	57382	A	27177	79	1241	
27015	57383	A	27178	3	299	



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26982	57350	A	27139	210	291	
26983	57351	A	27140	395	680	
26984	57352	A	27141	157	485	
26985	57353	A	27142	1	507	
26986	57354	A	27143	1	1041	
26987	57355	A	27144	1	671	GASGAAAYGADMAKSKNHTT HNQSRKWHNRNGIKKPRSQRYE SLKGVDPKFLRNMRFAKKHNK KGLKKMQANNAKAMSARAEA IKALVKPKEVKPKIPKGVSRKL\ DRLAYIAHPKEGKRARARIAKG LRLCRPKAKAKDQTKAQAAAP PSVPAQAPKDKDTSNIFISNRKR GCDFTKKETNIPKVLTISMAPSL MSLYSVTRNQTTKPPSRHKNLT KGQLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	A	27147	1	675	
26991	57359	A	27148	142	456	
26992	57360	A	27149	3	175	
26993	57361	C	27150	378	434	
26994	57362	A	27151	1	792	
26995	57363	A	27152	1	578	MVRCVRLVEAGSVVRYLSTSIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIA YVRARELHTLEVTGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI
26996	57364	A	27153	1239	1905	SAAAAPATGVPACRAGAWVSA APPAEGRPARARRHPGRCLEAA GPRGQRGA AHGH*ARAGSPQP GAPPCHPLGIPARQPLGLPRRTR CFGGIAQRGRAARHCLLSRPSA KAKRNSSYREPGMGWRSPQA LGEYGKGSQAGSARLSGAASQ GRRARHLRGKAPAWNPPPPSP PPPALGLPLRTQREATRKPRRE EARRPRPRPLRPGGANGSPGPP RAARA
26997	57365	A	27154	1	1275	
26998	57366	A	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL VGLWSH
26999	57367	A	27156	2	367	
27000	57368	A	27157	98	293	GQTFATASISLLRYATGCGVFP RV*IRSPRAIPALSGDWPAFVS LSEPPRFVCLRAMTKAAAF
27001	57369	A	27158	3	211	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26971	57339	A	27128	240	719	HSKKLVTLSHGVSMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LPEHDGFCYIHVAQSAEITGLTS GNPVRIYGRH*RVSRGRKVVL YRPEEDAGDEKGYESFPWVIKR AHRPSRGLFSGHIPPIHSLLYR
26972	57340	A	27129	1505	3812	
26973	57341	A	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	A	27133	183	524	MSTPRPPFVPAFVGRRPSLLFVP AARLTDVVRGRKVRACGLLSPR LRSPSSSSATRVARHSIGRPRVA RLSTVFVAVCVESPSRQRRWCL FALAATPRAPGTLA*SCLTDSFS A
26977	57345	A	27134	1	1025	MIFVLQIRVRGHDDSFLLKNHLV FLVIYGTNGTFNQTLVTDNNGL APFTLETSGWNGTDVSLEGKFQ MEDLVYNPEQVPRYYQNAYLH LRPFYSTTRSFLGIHRLNGPLKC GQPQEVLDYYIDPADASPDQE ISFSYYLIGKGSVMGQKHLN SKKKGLKASFSLSTFTSRLAPD PSLVIYAIFPSGGVVADKIQFSV EMCFDNQGTDLTSTVRVTRSSA SVMVYGASEAIGQRQSSAAKP RRSQSDSLGPEFQGLWERLPGL RINGELITAYPQVVVRVPTPW VQSDSDITVLRHLEKMGCRML NRPQAILNCVNKFWTFQELAG HGVPLPDTFSYGGHENFAKMID EAEVLEFPMVVKNTRGHRGMY ELLVSTMGCSNSGMVTTPIKWL SMISVQCLANGTFLSPSLTKCPK GIRASVPLSGGPRSLKARTFSAF SGPVRSDQAELPEAYEPIEV NEFGEIDLLAMVEDEIILALPVV PVHDSEHCEVSEADMVFGELPE EAQKPNPFVAVLASLKRVRMA VQQNKPTRSKRGMRRSHDALT AVTSLSDKTSGEKHLRHH*SA DLAAAPRAPGTLAQGCLTDSFS
26978	57346	A	27135	79	306	SGDLPWEINPLSSCSLLREKDP MTSGPQTNQPKHLINFKSGPH WKSDCSTHLAATPKAPGTLAQ GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	C	27137	63	370	
26981	57349	C	27138	107	408	

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26965	57333	A	27122	916	1568	HHSHEQQFQWPVGASGVDRW AGYLHQFRSLTQFQYGAEPDR KE* CQIFIMQKTLSCLSILGKR TMSLMQ
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCFVIFRH RYLFAISSWSGVTVAIRKDRES ADLGSDGQNGQDLWDGGGAA AADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
26967	57335	A	27124	606	852	HQILFDRTPVSVDDQSVEKKG*D HSVRPQ* AAPGHVHYLTIPEKS SQHYHPRTTSE* TSGRYESSGG LSFSQCMRGALEFCC
26968	57336	A	27125	1	2680	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVVDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPAETSQGAL GTLANVVTSLANLSESLNNGDT SEIQPEDQSASEITRAFDTLAKA LNTDSSSSPSLADGIDTSGGGS IHVISRDQSTPIIEVEGPLLSDTH VTFKSIREDRNGRSQKTVHTEG DMNMNIKKIVKQATVLTFTTA LLAGGATQAFKENNQKAYKE TYGVSHITRHDMLQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTVAEYNGY HVVFALAGSPKDADDTSIYMF YQKVGDNISDSWKNAGR VFKD SDKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYLVEANTGTENGYQGEE
26969	57337	A	27126	2014	2138	LSCSGWRAG**ADGCIIQIG*RL SPNKCL* TWSALCNPTAE
26970	57338	B	27127	1	7616	

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26953	57321	A	27110	1	2047	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFQTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPHLMRLAIETVAHDYDVI VIDSAPNLGIGTINVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKTVDLKGFEVDVRIILLTKYS NSNGSQSPWMEEQIRDAWGSM VLKNVVRETDEVGKGQIRMRT VFEQAIDQRSSTDTSLSIPAAP MVDSLIARVGVMAAGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSPHGELSARSGDALQ KAFTDKEELLKQASNLHEQK KAGVIFEAEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMALNLDNRVPAYIIRSYIR CGRKGFASAGVGGCRGWLNY AASEQIVLRVHHMRCEIPHRCV
26954	57322	A	27111	1175	1298	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26955	57323	B	27112	1	1056	
26956	57324	A	27113	1979	2217	WLSVRVDGGANSGLGKHGSK KCCT*NG*SW*RSDPDENCF*T EQ*STLFN\GAWRNALSIWEPV CN/GNFRSSD*TTLGD
26957	57325	B	27114	320	1633	
26958	57326	A	27115	606	705	
26959	57327	B	27116	1	4118	
26960	57328	A	27117	4048	4051	
26961	57329	A	27118	1791	1884	ADGCIIQIG*RLSPNKCL*TWSA LCKPIAE
26962	57330	B	27119	1	2436	
26963	57331	A	27120	1	2449	
26964	57332	B	27121	173	4112	

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26949	57317	A	27106	1688	2187	SYFIMVKVGTSTYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLWDWGGG\AA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS INSTEYTKVFALDVAARHRV QFAMPESDAVAMLSF
26950	57318	A	27107	782	1402	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLIKLLFYKIPSMVL SSVLLLEVKSHIVGPGLPGINRD TRIYLFCEVIFRHRYLFAISSWS GVTVA\RKDRESADLGSDGQN GQDLWDWGGG\AAAAADGVTFS VPVTPHTFRHSYAMHMLYAGI PLKVLQSLMGHKSISSTEYTK VFALDVAARHRVQFAMPESDA VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSISHSV GTRDLSRVSTILSPLYNTVAPG AN*CRELKLVLDDADDVLSTEVI RVITSSA
26952	57320	B	27109	1	934	

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26928	57296	A	27085	1	1439	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFFRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRV WTPGINCPGPCGVWTPGINCP GAWGIHGPHGSAENTGPLHPG QTSAQLETSLPLSLRSARELELA QLSPRRKQNRSLQNIQVTPSLR VPWPKASNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIIELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLFSDSRGSKMTIDV PQAKSNNVGITSYMTNRSFFED/ KKATFAPGFLWNIAIKTS
26929	57297	A	27086	345	563	
26930	57298	A	27087	1	1188	
26931	57299	B	27088	1	1186	
26932	57300	B	27089	1	1090	
26933	57301	A	27090	183	410	
26934	57302	A	27091	1	1557	
26935	57303	A	27092	888	1165	CTRERRIKARGPPAGKRWLLLS GSSGRKHHL*QDPRPGSQTAGD LPEPARPIIVIGEGSQMGLDECQ FQFRNGRWNCALGERTVFGK ELKV
26936	57304	B	27093	1	1027	
26937	57305	B	27094	1	1117	
26938	57306	B	27095	1	1377	
26939	57307	B	27096	1	1014	
26940	57308	A	27097	1040	1285	
26941	57309	A	27098	901	2277	
26942	57310	A	27099	1	1122	
26943	57311	A	27100	1	1137	
26944	57312	A	27101	1	1881	
26945	57313	B	27102	1	1211	
26946	57314	A	27103	294	506	NRRPGSAATVWAAAAEPSE NNPALENR*SSGFSWGFFSGYQ RCRESRATTAPGYGNSRTG*AT CWLYN
26947	57315	B	27104	1	1073	
26948	57316	A	27105	1	1809	

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26916	57284	B	27073	1	1116	
26917	57285	A	27074	1	1173	
26918	57286	A	27075	1	999	
26919	57287	A	27076	771	908	
26920	57288	A	27077	104	547	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLKFLKNGLNFLHHSVGTDRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS
26921	57289	A	27078	34	1353	
26922	57290	A	27079	213	338	LSCSGWRAG**ADGCIQIG*RL SPNKCL*TWSALCKPIAE
26923	57291	A	27080	1	1246	MVKVGTSYVPINVSFSPKVGPG LPGINRDTRIYLFCEVIFRHRKD RESADLGSDGQNGRPWIGEA VAAAAADGVTFSPVPTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRNRFTQFRLSETKEITNPYAM RLYESLCQYRKP DGSCIVSLKID WIERYQLPQSYQLYYFELAIPV GYFYPGSFSTASRILLHPRGLR AITIAVFGKQNTYIRLEPFKINV LEQITKHIEKLQCGGVVKQLSR RGNNQHISSTYDINRADYPG*A RDPHMLRLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEVDVRILLTKYSN SNGSQSPWMEEQNSGCRGKTS RVEVPHRDSQFKVIKLVTLRQL VTLYDPVDFQRDDA
26924	57292	B	27081	1	1041	
26925	57293	A	27082	1	1011	
26926	57294	A	27083	2	1007	
26927	57295	A	27084	1	738	

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26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGNYSNGDNHTLR/DPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQSSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG YVSNSLTGPYKPLNKTGLVLQ MVLIPNDVTFTYSIHFAVPQAK GNNVGIHQATLTNRGF FEIKKA TFAPSL
26900	57268	A	27057	66	197	
26901	57269	A	27058	379	905	AGNFVHITVRKMLWIRRDQQQ S/DKQDIQTAHRSYVLKGYND MYYGWPCCKVNEISGQLASEP A*SLVLPAAAG*QAPASGSPWLS GGPQQVEDAGAGYGFAPGQPP PPPRTQPRSACSRRAAGSQFHG RPLLPRQAAKARAPRSLGCGSL GRFSTGVRPDKCIFPETENAA
26902	57270	A	27059	1	1608	
26903	57271	B	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFGVANDPILKDQT QEWS\GSAPFTS\DGKFRIFYTD YSGKHYGKQSLTTAQNQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTPFFRKESQK LQSSAKKRDAELANGALGIIEL NNDYTLKKVMKPLITSNT
26905	57273	A	27062	1	3066	
26906	57274	A	27063	1	972	
26907	57275	A	27064	14	273	
26908	57276	A	27065	42	302	
26909	57277	A	27066	1	487	MGLSLKGPESAPIPKTPQFNKIL FKPIAVYNRFTQFRLSETKEITN PYAMRLYESLCQYQRYQLPQS YQR\SLTSAASCRSVLMRSTA ELQCASHTLRKRKAARRLISLS EMPRKQGDYRTRIWK FEDGLS NVLVIQLNKLIIICVMCLVRDCD VLKTYFHR
26910	57278	B	27067	1	1035	
26911	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG** C*EDLSGMVR
26912	57280	A	27069	1	2784	
26913	57281	A	27070	855	980	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26914	57282	B	27071	85	863	
26915	57283	A	27072	345	500	



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26884	57252	A	27040	347	1061	
26885	57253	A	27041	212	386	LQGSWVTSGLERICGSILGTIPL AHEVTDQTQHGRMVYQVATAG F*SSLGAASIGTQGL
26886	57254	A	27042	1	1017	MHSRRERARGRLRGAHHPLVDN GPPQSLRAPPLSPLKTAGAKSI WEPLASARRPETPERTPLQKTP EQVPTNFMGALHMKTSAPLSS RNGEGRRGGTSVASC PWVGA VCSAERQPCTQRVREALMGGW RAGAQQNRÆEDQVDEFTEVGF RRWVIKNYDELKEHVLQTCKE VKNLDKSIHPEISRLHEFITTTHT LPVIGGKVSLLSKCQDNAEQKQ SQGCSQEGHEVYDPRLNSSSSS SSSGGGQSPGLRRCSTSAAAAA ALEGAALKPMPVHAGLVGSGE GGGAGAVAGPCSRWGATTAA ASSAQAQPVRRGGSSGAQGHR GGRRRQAGKGGPAG*TAAAAA AP\GRGAEPGAAALLNLGGGSG GAGSAALKPMPVHAGLVGSG EGGAGAVAGPCSRWGATTAA AASSAQAQPVRRGGSSGAQGH RGRRRQAGKGGPAGSS
26887	57255	A	27043	644	949	
26888	57256	A	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSIILPTPLEIHKV*IQIY A*GCKRISNNCWHCHQHLLSIS PDLRINEGKECGSPWIGVEAR/ MGELSSAVGLTSLLLYQQVPF HPHFQSPTFIPRESILLQHASCW RQHHLHTGIYSSYLPGWKQEF
26890	57258	A	27047	1	2445	
26891	57259	A	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	A	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI* RSTLETANSISARLNNPFLRKYP SYFSLFMGTTRI
26894	57262	A	27051	277	394	
26895	57263	A	27052	2	1394	
26896	57264	A	27053	1	1091	
26897	57265	A	27054	1	1404	
26898	57266	A	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ SAG*RH*DRN*DGNQY*SR/SLS *SR*STTK*RNTPCSQVSSLSRLS TRSA

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26875	57243	A	27031	2	1019	PTSAPHSLSPRAVIERRSRALDW NASPSLSDPQGLDASLPFPSHKR SRTASPEPAEHPVMDKNELVH KAKLAE\QAERYDDMAACMK VT\EQGAELSNEERNL\LSVAYK N\VVG\ARRSSW\RVVS\SIEQKT EGA\EKKQQMAR\EYREEIETEL R\DI\CNDVLSLVGKSSLIPNAFT SRRSKVF/YILENGKGDYLPFTL GWRVAAGWMDQERGLFDPVH NKA YPRK\AFWKS\AKKGNGNPT HP\IRLGL\ALNFSVFYYEILNSP EKACSLAKTAFDEAIAELDTLS EESYKDSTLIMQLLRDNFDIVG HRDTQGRRKLEGREEGRGENL TGPFTFCSWPHS
26876	57244	A	27032	177	477	
26877	57245	A	27033	1	1290	
26878	57246	B	27034	49	1112	
26879	57247	A	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	
26882	57250	A	27038	1	440	MKMRVGCMLTAESLSDGGNS HQRTLSLFEESKESQCEARGEV SKAGVWLVPLEPSSDALPKITS LVRPAVPWRPSSEAGLCEVRGG VLGKASKAPIKEPQLDRGMGL GAQRRGSSGTEVQSGETLGASG SPRGLLEPRPDWVSNNAGSLG FQQLPIVDKIRTIAQAVCGAKDI ELCPEAQVKIDRYTQQYYSC*N PKLPAPLFETQSGLGSKSPLGLP LAPRVSPDCTSVP/GAP/SAAGP RAPCPDPAVAPLWGLCWPFPEL
26883	57251	A	27039	1	1113	MHQEDLRAWYLDLGLPSHQN AQPTAWKCQRAPSPYTHQDMA LIPSPTARWLSPEKEPKQGEVG EKSLLPDPTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRL\ADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIILCTLVNKLQPGSVP KIN\ASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLALAGKAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVIRLQITNKCASQSGMT AYGTRRHLYPDKNRILPPMDNS TISLQMGTNKCASQVGMTAPG TQRHIYDTKLIDKCENSSMSL

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26862	57230	A	27015	53	1227	QPPVHTTPASSPCDD\DIAAL\VDN\GSGMCK\AGFAGDDAPRAVFPSIVGRPRHQGV\VMGMGQKDSYVGDEAQS\KR\GILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLDPRATREKMTQIMFETFNTPAMYVAIQ\AVLSL\YASG/RVTTGIVMDSGDGV\THT\VPYIEG\YALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYQLPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSIMKCDVDIRKDLYANTVLSGGTNMYPGIADRMQKEITALAPSTMKIKIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNCVVSSCQPPAFLVLFSSSRLPAGEGRGRPGQTQRPSSEGA\WHSVTLERRCLVSHLINLREAGMYPSPRCHHLFPDQLV*TEGGF*RPRLGWQRCHGTPQQA\PSQPAFRSKHPRKGMPALQQPGSGLCRPLPCR
26864	57232	A	27017	112	493	AHSRTPARPENRAAASAPRKPRRAMSSPPEGKLETKAGHP\PAVKAGGMRIVQKHPHTGDTKEEKDKDDQEWESPPPKPTVFISGVIARGDKDFRPADAQVAHQKPHAS\MDKHPSRPTQHIQQPRK
26865	57233	A	27018	1	1176	
26866	57234	A	27019	3	307	
26867	57235	A	27020	86	179	SVKRRCSLLTWIGMRLQRQHRECLAEQVGS
26868	57236	A	27021	1	948	
26869	57237	A	27022	3	534	EGAHFRAAHHPSTGSRCPGSLQPSRPLVANWLQSLPEMPVDFTGYWKMLVNENFEEYLRALDVNVALRKI/APTLKPDKEIVQGDHMIIRTLSTFRKLT\SWNFQVQKKEFEEDLTGIDDRKVHDKQ*AWDGDKLQCVQKGEKEGRGW\TQWIEGDELHLEMRVEGLVC\KQVF\KKVQ
26870	57238	A	27026	1	2400	
26871	57239	A	27027	294	425	
26872	57240	A	27028	1	797	
26873	57241	A	27029	1	173	
26874	57242	A	27030	1	1047	

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26845	57213	A	26998	2	514	VTARRRGTRWLRFRRASRVQK WLWLADFYLRYYVGHKGKFG HEFLEFEFRPDGKLRVANNH YKNDVMIRKEAYVHKSVMEE KRIIDDSEITK\EDDALWPPDR VGRQELEIVIGDEHISFTTSKIG SLIDVNQSKDPEGLRVFYLVQ DLKCLVFSLIGLHFKIKPI
26846	57214	A	26999	1	570	
26847	57215	A	27000	1	980	
26848	57216	A	27001	270	356	
26849	57217	A	27002	1	1032	
26850	57218	A	27003	1	1017	
26851	57219	A	27004	1	450	
26852	57220	A	27005	1	637	APIECGGIPSLPVLCSRANDQE GVRLLPESEAMPKSKELVSSSS GSDSDSEVDKLLKRKK\QV\AS ENPVKK\QKTGETS\RALSS\SKQ SQPAARDNMFQIGKMRYVS V\RDfKRQKCL\NDIREYWMDE GEMKPGRKGISLNP\QQWEP SLKEQISGPLIDASKKTCKISEPIL IKPCTVPVVL\IWLFSIGFCFLNVL RSYCMFGLQKNL
26853	57221	A	27006	20	412	RFSPLSFLLAGDSCTCAGSCKC KECKCTSCCKSKWDPLFPLPLP CPPACPLSTILRGIAVWGCP IA RKLLPPQ*SLSGRAGILIPG VAS THLCRLLSAPR\CCSCCPV GCAK CAQGCICKGASDKCSCCA
26854	57222	C	27007	32	505	
26855	57223	A	27008	854	1021	ALGGVAEYDLKEGLLLKH*AL VQSLVATEVRLVLCITSHTDML QICFFVYATVTQ
26856	57224	A	27009	1	726	
26857	57225	A	27010	99	537	
26858	57226	A	27011	1	963	
26859	57227	A	27012	146	609	VYLRCTGGEVGATSALAPKIGP LGLSPKKVGDDIAKATGDWKG LRITVKLTIQNRQAQIEVVPSAS ALIIKALK\EPDRDRKKQKNIKH SGNITFDEIVNIARQMRHSLAR ELSGTIKEILGTAQSVGCNVDG RHPHDIIDDINS GAVECPAS
26860	57228	A	27013	3	501	
26861	57229	A	27014	1	1623	

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26825	57193	A	26978	3	450	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTTEPQQPGVPPPEPP PTGACYTCRKSGHWAKECPQP GIPP\NHVPSVWDPTENLTVQLT WQPLPEPLELWPKAL
26826	57194	A	26979	615	724	
26827	57195	A	26980	1	1968	
26828	57196	A	26981	227	556	
26829	57197	A	26982	400	548	
26830	57198	A	26983	1	1968	
26831	57199	A	26984	65	741	
26832	57200	A	26985	1	658	
26833	57201	A	26986	1	666	
26834	57202	A	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA VIREETFDGWHPQDRPLPAHA\ LVAG\IDRPTPPQK*TAAMGKK KDRPKRSKIKSFCGKCYN\NH\ LMPHKGTLDIPLGQNLFFVQL RDVFRDPGSLNRKARREGPRF KFE/EREYETGQETKWVLPKRL AGFKNAFGFDSLKIIKKKKKKK KTTTKKGRP
26835	57203	A	26988	1	352	
26836	57204	A	26989	1	1419	
26837	57205	A	26990	2	878	
26838	57206	B	26991	75	2931	
26839	57207	A	26992	229	724	IIFIVYSSQLTYVKISDSFQTFKF CLDFCLFFSEMS\FLSLNISSCS* YSAKVNSCGKFGLTKGSFSAPL TPLFFLCFSELVEGV*ELLAVG GLHLARIFLCLSISSLC*FTHSCC FTRVTPINLASNNSCLLGFRQLQS SSIAPSLGLLDGGVCFIRDIAAA
26840	57208	A	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL KLSN*NMTSVQQFTIELEGNLS LSCIELVC/ILVTHCHLF/CMNK AW*QKKNT/WLSILTC*KHWQ YYNLVNSTDFNTSSSFLSKV
26841	57209	A	26994	1	1209	
26842	57210	A	26995	2	1683	
26843	57211	A	26996	1	1386	
26844	57212	A	26997	1	471	

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26798	57166	A	26951	224	475	AGPRKMAPSALLRPLSRLAPARLPSGPSVR/STKFFVREPPNAK PADWLKVGFTLGTTVFLWIYLIKQH\NEDILEYKRRNGLE
26799	57167	A	26952	1	411	
26800	57168	A	26953	442	2490	
26801	57169	A	26954	3	1592	
26802	57170	A	26955	9	308	
26803	57171	A	26956	153	227	
26804	57172	A	26957	1	411	
26805	57173	A	26958	517	825	
26806	57174	A	26959	6	646	
26807	57175	A	26960	1	275	
26808	57176	A	26961	3	272	
26809	57177	A	26962	1	1002	
26810	57178	A	26963	1	1791	
26811	57179	A	26964	2	160	HMTTSLAQSGFQKTSALNKIT TKGSH*VQFTSLLPPPERVLVS MAERPWGG
26812	57180	A	26965	1	892	
26813	57181	A	26966	1	549	
26814	57182	A	26967	234	387	SCLEVCDEQGPEK\TRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL
26815	57183	A	26968	269	501	RARSEGAGLWSVVAPSAVSVFF VSDPRCAPFHRSPPCCSP/RRPC LSLSA*SRPRASGVGACLLWQP LPEPELWPKAV
26816	57184	A	26969	210	296	
26817	57185	A	26970	71	283	LRLGDLPSEINPLSSCSLLREKD PPTSGPQTTSPRNISPISNPDEST GNRTVQLTWQPLPEPELWPK AL
26818	57186	A	26971	1112	1180	
26819	57187	A	26972	71	284	LILGDLPSEIKPLPSCSLLREKEP PPTSGPQTTSPRNISPISNPDEST NRTVQLTWQPLPEPELWPKA
26820	57188	B	26973	1	663	
26821	57189	A	26974	1	502	MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLGDKSPVLLLFALER QRRHVLSMDPKLRCWSRTGKA AFPWCLIIAEMPDYSPTFQRCQ TTQGRLPWSFTLSSKSRFSGEG ARACYKCQKSDHQAKECPQPG IPPKPCPICAGP\TGNRTVQLTW QPLPEPELWPKAL
26822	57190	A	26975	233	496	
26823	57191	A	26976	226	543	
26824	57192	A	26977	1478	1744	

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26771	57139	A	26924	804	1100	SPKGGPPDPSHGTFHRSRCEET TKQAFCEQHGCLFHLGTLGALL G*QRWLHQLSRPSLGCNESKSL FQ*PPLP*E*KEIQCKVPPNLGL GVRSGKGF
26772	57140	A	26925	3	1186	
26773	57141	A	26926	126	363	SRSKDQGLDPSGTWCKRAFSPG PWPIIPVAAGGGGHSGGGKSET PAHLQKGLHKVKNC*PSTYSVC QTPDAEHPVSNK
26774	57142	A	26927	1	1125	
26775	57143	A	26928	401	446	
26776	57144	A	26929	332	499	
26777	57145	A	26930	74	200	
26778	57146	A	26931	300	416	
26779	57147	A	26932	324	430	
26780	57148	A	26933	60	381	
26781	57149	A	26934	2344	2453	
26782	57150	A	26935	131	274	
26783	57151	A	26936	144	444	GGGENFSYPWYLLVCGWGFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK
26784	57152	A	26937	540	811	
26785	57153	A	26938	69	375	QHLRPAAVAAATMPKRKAEGD AKGDKAKVKDEPQRRSARLSA KPAPPKPEPKPKKAPAKKGEKV PKGKKGKADAGKEGNNPAEN GDAKTDQAQKAEGAGDAK
26786	57154	A	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP GGSASAARKPTG/SPGREGAGR RGQWGPNNCCAGRLPGGESTV
26787	57155	A	26940	248	613	
26788	57156	C	26941	94	234	
26789	57157	A	26942	2157	2408	
26790	57158	A	26943	547	815	
26791	57159	A	26944	254	467	VFLISVYNGLAISLYLGIHIRQK PVMPRNPLNCFGVLG*G*AGIG *IRSSLRTLVLPLDNFSPKYLTC EQS
26792	57160	A	26945	238	391	
26793	57161	A	26946	232	1659	
26794	57162	A	26947	1	951	
26795	57163	A	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV GFTLSVEL*M
26797	57165	A	26950	1	828	

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26756	57124	A	26909	2	687	GARQVLPGESPCFSSSAKIVKP NGEKP\DEFESG/LSPQALLEL\E MNSDLKA\QLREPELLRPA*GK LKVGGCSENLSI/ILLFPVPSN*K SFPENPQVRA*YRELEKK\FQW GSHVGLYRPQRRILP*AQLRKK PVQKNKQKASPRARTLTAVHD AILEDLGLPQAKIVGARES RVK LADGSRLAIKVHLDKVAQQNNVE HKV\ETFSGVYK\KLTGKDVNF EFPRSFNCKQK
26757	57125	C	26910	164	208	
26758	57126	A	26911	2288	2625	GSEGLPITKRWSSLWEWRKG LSEVGSKRNLVRCLRTAI/LM GGEAGVIHCKGHQKASDPALG NAYADKVARQAASSPTSVPHG QFFSFTLVTPYSPAETSTYQSL PTQ GK
26759	57127	A	26912	1	400	
26760	57128	A	26913	3	277	
26761	57129	A	26914	1	630	CEIKNRKAAEKVNKTKGKFFEI NTYPGPIKTGEPGSGQTQKWLDI VRNTLVEEDTSSWSWRAHQPK STLTGTGRPSTNGTMSSLARTV REEPGNQPNYRGKPSFPWFPHL VRAASTQPVITRLLQHGRLLKPI NSPYNFPILPVLKPKDPYKLVQ DLHLINQIVLPIHPVVPNPYTLL SSIPASTTHYSVLDLKHAFFTIPL HP*FQPLFTF
26762	57130	A	26915	1	384	
26763	57131	A	26916	1113	1319	GRDPVSAFYIWLASFNPNTIY*IG NPFPIACFSQVCQRSDSCRYAA LFLRALFCSIDL YLCFGTSTMLF
26764	57132	A	26917	2	2144	
26765	57133	A	26918	99	470	
26766	57134	A	26919	636	1220	GPGFQAQNCAAIWADTKLAAG IFSHTPVAPGTVPVRQNHLLPWD APAWSGEECLPLRLVYVVFPS QCKQSCQEV*TGQSPPLGKAF VARLPL*IPSLWAGHLFLEHPV YCCGCVTAGRQGSWKQRRH GHPFPLPLLLLQMVCCSISYQY DYPESSFLLLFLSSLCSAGKSTG SHAILLGSFAVLPHLVALRS
26767	57135	A	26920	10	161	RLRMVRDIKVLNTRSLRNLG DLTNKGRSII GPPL*ELSKASVM VPVGF
26768	57136	A	26921	1	855	
26769	57137	A	26922	5	1442	
26770	57138	A	26923	1061	2332	



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26733	57101	A	26886	1	1371	MSFLIDSSIMITSQILFFGFWLFFMRQLFKDYEIRQYVVQVIFSVTFAPSCTMFELIIFEILGVLNSSSRYFHWKMNLVCVILLIL/VFPMVPFLQLAYFIVSNIRLL\HKQRLLFSCLLWLTFMYFFWKLGDPPILSPKHGILSIEQLISRVGVIGVTL MALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTASGSENLTLIQQEVDAL EELSRLFLETA DLYATKERIEYSKTFKGKYFNLGYFFSIYCVWKIFMATINIVFD RVGKTDPVTRGIEITVNYLGIQF DVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQIMGMYFVSSVLLIRMSMPL EYRTIITEVLGELQFNFYHRWFDVIFLVSA LSSILFLYLAHKQAP
26734	57102	A	26887	1738	2140	
26735	57103	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	A	26891	113	367	
26739	57107	A	26892	2	1391	
26740	57108	A	26893	154	647	
26741	57109	A	26894	40	747	
26742	57110	A	26895	1	3186	
26743	57111	A	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	A	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	A	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	A	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	A	26905	3	156	
26753	57121	A	26906	2	397	VDGMGWSQDLFRALGRSL SREGKEHVGTDQFGNKYY*SRSTKTGEVRWRRGQRLRGQ*LRGQTI REKRIVEAANKKEVDYEAGDIPTEWEAWIKRTRKTPPFME EILKNEKHREEIKIKSQDFYEKEKL
26754	57122	A	26907	1	1350	
26755	57123	A	26908	1	582	

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26719	57087	A	26871	171	495	SQLLDMRKPFQKPGRLRLKTL QYLNTR/CILDYLDNISPPQIRK LFYVLSTLAFSKQNEASSHIQD DMHLVIRKQLSSTVFKYKLIGII GAVTMAGIMAADRSESPSL
26720	57088	A	26872	1	3114	
26721	57089	A	26873	173	397	
26722	57090	A	26875	823	1194	
26723	57091	A	26876	1	1263	MESNAVQLTRMEYAMKSLSL YPKSLSRHVSVRTSVVTQQLS EPSPKAPRARPCRVSTADRSVR KGIMAYSLEDLLKVRDTLML ADKPFFLVLEEDGTTVETEEYF QALAGDTVFMVLQKGQKWQP PSEQGT*WRRTRQRKDSPVSRPC STHGLQEIQ
26724	57092	A	26877	128	317	
26725	57093	A	26878	431	574	
26726	57094	A	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD WEPAFSEDGRARTVARLQHPPL GGPTRYHHFLRRHDPPLRVHP AAERQEAHPGTSI*QSSPNSKQS PQGWKITFPNSLSLTRKYFYFQ QPRGWDFFKKT
26727	57095	A	26880	3	179	
26728	57096	A	26881	977	1127	
26729	57097	A	26882	121	708	
26730	57098	A	26883	38	828	GSRLRRLQAAAARPALPLPLPP WEWKHLPHVPEAKWWLTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESDLAEFAK KQPWWRKLFQGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATACGEVDF/LLQLANH TWVHQS LTGNEWKDIIESPKS SLKIRKSQSDYLLRSGAKAAGR WCHFVKKNVLVTWGIFPEAFC LAWHPKEDDLHVPLFPGFPSQ QPFTLHHRDIESLLLFPWPSFP GHWEN
26731	57099	A	26884	1	642	
26732	57100	A	26885	1183	1349	

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26707	57075	A	26859	2	640	EARGROPQLHHLPHPPRASSPP LALQPLGRSRRCPPPPGAAAPD PRPDMGDLPLGLVRLSIALRIQPN DGPVIFYKVDGQRFQGNRTIKLL TGSSYKVEVKIKPSTLQVENISI GGVLGPLELKSKEPDGDRVY TGTYDTEGVTPTKSGERIQPIQI TMPFTDIGTFETVWQVKFYNY HKRDHCQWGSFVSIEYECKPN ETRSLMWVNKESFL
26708	57076	A	26860	218	426	TQPRVWSQAQ/RALQPDTELPQ PPQTPKSDTDQMLSVKKKKKKR KKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKLYFQT
26709	57077	A	26861	1	423	
26710	57078	B	26862	1	252	
26711	57079	A	26863	1	171	
26712	57080	A	26864	5	254	
26713	57081	A	26865	16	220	ILDTSPMRWTQKNFSMILAQPE QQCKTSLSQNKNDRIKKKEE KKKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKKKEKE EEKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKK KKK
26714	57082	A	26866	32	286	
26715	57083	A	26867	1	847	EVKDLYDKTFKSLKKEIKEDLR RWKDLPCSWIGRINIVKMAILP KAIYRFNAIPIKIPTQFFNELEGA ICKFIWNNKKPRIAKTLLKDKR TSGGITMPDLKLYYRAIVIKTA WYWYRDRQVDQWNRIEDPEM NPHTYGHILFDKGAKTIQWKK DSIFNNWCWHNWLLSCRRMRI DPYLSPECTVKVSKWIKELHIKP ETLKLIEEKVGKSLEDMGTER FLNRTAMACSKKKEKEKEEED EEEKEKEKEKEKEKEEKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKK
26716	57084	A	26868	1	376	MLMKDPQWNSSIFISTHLALQQ KRRQAEYGAQEPSRRIVGGKGS GAQVDEEEEEEEEEKEEKK KKKEKRRKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKMML LSLPMIRPLPHPRWASSPSSMV AKP
26717	57085	A	26869	1	2031	
26718	57086	A	26870	1	957	

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26697	57065	A	26849	136	3261	PMSPTIYDIARVAGVSKSTVSR VLNKQTNISPEAREKVLRAIEEL QYQPNKLARALTSSGFDIMVI STRSTKTTAGNPFLLEVAQAFP AKAE*KGQVLVRTSHNPAEDL QKCESKIKQKMIKGII MLSSPAD ESFFAQLDKYDIPVVVIGKVEG QYAHVYSVDTDNFGDSIALTD ALIESGHQNIAC LHAPLDVHVS VDRVNGYKQSLGAHNIAVRDE WIVDGGYTHETALKAARQLLS QSVSLSVAVSW SAC
26698	57066	A	26850	73	174	
26699	57067	A	26851	252	575	PGFPRGPPPPPGFAPFHVSIWDT DLSDPAARAGLGVRWTPDPPR RAARSPVLPRGLSAGQRP AARL LGMEEGRFRQVAVFSES*SAV CPPSPPPLSPLAPWTETA
26700	57068	A	26852	1	462	AQSVNSQTFSEL RATQTFYKTT SHNSPGVFHTSTKR FIDGNPPGI FSAITA*RLMMP*RSSIFSASASI LSVSFSGSTCNNDQRP ARFGVL *DTRGETGCA*TGRPRRAR*LR RVEVRAV*LLRVRARNGA QMA LVKTPCQTSAHNAPCRGRE
26701	57069	A	26853	692	918	
26702	57070	A	26854	1	2427	
26703	57071	A	26855	1347	1978	LPHCVANHGCALR*QKWVHD KEQTTQTLKMVAENGRWVIDD IVSNHGSVLQAVNSENEKTLAA LASLQKEQPEAFVAELFEHIAD YSWPWTWVVS DSYRQAVNAF YKTTFKTANNPDEDMQIERQFI YDNPICFGEESLFSRVDEIRVLE KTADSARIHVRFTLTNGNNEEQ ELVLQRREGKWEIADFIRPNSG SLLKQIEAKTAARLKQ
26704	57072	A	26856	1	733	LSEVDVDVRQSIHSAHAKTLDT QGLRNEFLVEKVFADEYTMV YSHIDRIIVGGIMPITKTVSVGG EVGKQLGVS YFLT SNRRRTINKY LVPDVLETCQSSMGLTELAPGN *WNTMPCHTHERRMEVYFYFN MDDDACVFHMMGQPQETRHI VMHNEQAVISPSWSIHSGVGTK AYTFIWGMVGENQVFDDMDH VAVKDLRANHHRFIISQRSDI HLTTQWIKRAAQTIHPPVSIQQ IVAF FE
26705	57073	A	26857	2	255	
26706	57074	A	26858	1	597	

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26692	57060	A	26844	1	978	
26693	57061	A	26845	144	647	
26694	57062	A	26846	1642	2652	FGILVLLALIVIWYNNFFGAETE AILPYDQYMHRFAAYFQQGNM ESNGKYVDRNGNVVDYQTGP WGEPGTNGQHAFYQLIHQGTK MVPCDFIAPAITHNPLSDHHQK LLSNFFAQTEALAFGKSREVVE QEYRDQGKDPATLDYVVPFKV FEGNRPTK*ILLREITPFSKLN EYKASDITCIVRDGQHIGTRD GIEHLTAWHPVNRHIKRVNDVS FSLKRGEILGIAGLVGAGRTET IQCLFGVWPGQWEGKIYIDGKQ VDIRNCQQAIAQGIAMVPEDRK RDGIVPVMVAVGKNITLAALNK FTGISQLDDAAEQKCILSHPRCS WQGRHLLH
26695	57063	A	26847	52	137	
26696	57064	A	26848	1	1858	MGLKVDDKVPLFAVVSRLTSQ KGLDLVLEALPGLLEQGGQLA LLGAGDPVLQEGFLAAAAEYP GQVGQVQIGYHEAFSHRIMGGA DVILVPSRFEP CGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVFEDSNAWSLL RAIRRAFVLCQGQFHRTTDVE YKGDPAVKIEESEINYLNVY NTHFKKQLSRDDIVWTYSGVR PLCDDSDSPQAITRDYTLDIHD ENGKAPLLSVFGGKLTTRYKLA EHALEKLTPYYQGIGPAWTKES VLPGGAIEGDRDDYAARLRRR YPFLTESLARHYARTYGSNQRA ACSAMREREARTLPQKLAGTL GMLSKVMRIPRQQEVTALRTY LQIRIGLHAAFNACEEMCQRVA LERQLDSEERALLIERSQTVIRQ GRDLLHAWDATWNSAQALDN ALQPDRAGQFADALEKYAADE SFFAQLDKYDIPVVVIGKVEGQ YAHVYSVDTDNFGDSIALTDAL IESGHQNIACLHAPLDVHVSVD RVNGYKQSLAAHNI AVRDEWI VDGGYTHETALKAAARQLLSQS PLPEAVFATDSLKLMSIYRAAA EKNIAIPQQLAVRILFGLHL*IV LSTRAGFGNLAHY

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26682	57050	A	26834	179	876	CIVLFFFSQFN FVGRILGPRGLT ANVNRYLELHTLYGYMNL FIV SIMKDVLSL*RE*F*SCTL*IF*E EQNRGKPNWEHLNEDLHVLIT VEGV*I*LLYLWTVSNAFISCVF HV*AEGEDRYCCLYTSF*ISLLT VAALAFSLAATAQAAPRIITGP APVLPPAALRTPTPAGPTIMPLI RQIQTAVMPNGTPHPTAAIVPP GPEAGLIYTPYIYIISKYLWLLSS CSPEP
26683	57051	A	26835	3	915	AEAHPRLPDAADERQEAHDSLP NFCGIFNHLERLLDEEISRVRKD MYNDTLNGSTEKRSAELPDAV GPVQLQEKLYVPVKEYPDFNF VGRILGPRGLTAKQLEAETGCK IMVRGKGSMDKKKEEQNRG\ KPNWEHLNEDLHVLITV/EKV LQEQGQEIKLKRAVEEVKLLV PAAEGEDSLKKMHLMELAILN GTYRDANIKSPSLAFFLAGTAQ AAPRIITGPAPGLPPAALGTPTP AGPTIMALIRQIQTGGMPNGTP HPTAAIVPAGPEAGLRYTPYEY PYTLAPATSILEYPIEPSGCI
26684	57052	A	26836	1182	1360	KLSICVYIYICMFIYTHVSV*FYI YIYTHRHTENHYFCNSVQFVLY LFTFFCYFIWPA
26685	57053	A	26837	3	348	RNSKHVCRAEP*GHFCYK*HF WNHTEHTAVLEI/EQINARDET DF\YLGNRCTYVCKEQHSGPGS KSNTTIVIWGKVTCAQGKNSV VCAKFQSHPPAKAIGHRIHVML YHWRIQH
26686	57054	A	26838	264	527	NSKHVCRAVP*GHFC*K*HFW NQREHTTVLEIEGVYARDETEF YLGNRCTYVCKEQHSGPGSKS NKTRVIWGKERGSGWCRLSGR
26687	57055	B	26839	26	515	
26688	57056	A	26840	92	341	
26689	57057	A	26841	224	1111	
26690	57058	A	26842	2	592	HSLTGRCIFFLITGTSPGSPERMST TLKIMSSKEPSISPEIRSTVRNSP WKTPEITVPMETTVEPVTFSPQ LVFARLMTGVGLGAALPNLIAL TSEAAGPRFRGTAVSLMYCGV PIGAALAATLG FAGANLAWQT VFWVGGVVPLLVPLLMRWLP ESAVFAWRSISNKRA*FRDCRC CSAAIIW*RRFPFKSKPVM
26691	57059	A	26843	2	141	

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26672	57040	A	26824	89	554	AMNSCVTGDRYSPCGGFGFAF LYSSVSVSSESSEYQLSPLPPAKR PLAAQQSCSIPIASVFQQTIIHSLF AKDKKEFSSNLLDSKVNMCHE AHQLISHS*ANFRSICHIPQRW* NLIFEKFSVDVSMGSGTGF**AEN WS*TLSIAASLVYSLLHKKIQ
26673	57041	A	26825	84	239	ACTKKACYHHNHRYHHHHH HQTKP*QQELNSFRFSLSQPSLL AVFLFLRP
26674	57042	A	26826	2	245	
26675	57043	A	26827	154	546	LIVTVHVNHLGVLINHRFRISGC GVCCTDCISHKFGAADATGPS WTTHCAVITFSLTTGSATKKTE DNNTFVFNVVDVKAN*HQITRA VKKLCDIDVPEVNTLPNVVISFR FLLCSTVFCTLTVFFLRENG
26676	57044	A	26828	331	612	NHRGLPFPDYPGTYFLFFFFLF FSFSSFSSSSFSFPASGNHNSTLY FYGINFFSFHIGMRMGIFLCLT CFT*HDVLQAHPHREGRQDLLF HD
26677	57045	B	26829	928	1617	
26678	57046	A	26830	95	929	
26679	57047	A	26831	3	1128	LYNRRRRRRRCSHCRHRCRLSS GLRKEEVISLGASLGRVFPVPCSP PTVSAARGPTGAPGGPNSKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAAM KAVTEQGHLSNEERNLLSVA YKNVVGARRSSWRVISSIEQKT ERNEKKQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKCRLSNYFRYLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTL DI*P*QNSACVINFILFLNLRDN LTVSTTSTGFIVSFLFTYLIHCY LQEVCSVSLCTLNIYPLCDKKK
26680	57048	A	26832	139	601	EGRGHLAQELLSEVFVPCSP TGMTMDKSELVQAKLAEQAE RYDDMACSSERHVTEQGHE\LS NEEKKCSLVAYKECW*APRR\ SSWARVISSIEQKTERNVEGSSR WGKEYREKIEAELQDICNDVL ELLDKYLIPNATQPESKVFLK MK
26681	57049	A	26833	70	122	

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26664	57032	A	26816	299	707	RPPCRISCHPHTRCEGGRLRSRS PLLS*MPLSHPOGPSQPPAGSMS SSPPATTSTCSCSPPAAGCTRGR TTGRPFWTASGPAELDWASGSS VGL*SQGSQLGACGASYAGLG VPPRLLGPMTSCCMSLPFPSPAR P
26665	57033	A	26817	146	330	TVARRMELTPALLRALLNGILPI SEPPSNRIACWGKPAWTACCN SLRARR*RAISCCPSH
26666	57034	A	26818	1326	1694	IFGWFGACCSLGGSCCVFTAST CTTVCGGCAIKVGSCLSLATMG CCVCCTSGLGACSCWRGVSF* CLMESWGICGSLCWSWSACRW MVCFCLVWKHCRVFTCS*VCS SGGWLSFCCLADCD
26667	57035	A	26819	1	1407	
26668	57036	A	26820	75	1397	SRGSGREKFPAQLSYQTLLGKG PIEGTSLSNLAQQRCKEHHCHF LREQGPNCLIERFMDRYTGKYI HMASHTTRCRPHVSRPKARLL APATRSRSARARLRETRVRRGS PSCLWLNRRSRLPAEHSVRSP RDMVFESLGLPSTKSSEFRSAA PEAAERAQPGDPCGLQTPAPLR PGFRNQDPASAAAAAEEVRS GGGRGRILATTLWGCNTLCITQ YTRIRKLTLYCGVESKQEWG EYHEGVQAGLTRPGRSPKLISK FLEKELTDNRWDQEDEAEVK SSFPKND*VLKNRAIKKAKRRN VGFEVSAPLQLLLFKGLVPSG GGRFSGFGSGAGGKPLEGLSNG NNITSAPPFASAKAAADPKVAF GK*LPSPSRLLVDKVSNPKTNG DSQQPSSSGLASSKACVGNAYH KQLAALNCSVRDWIVKHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL HACHCP
26670	57038	A	26822	150	383	LCLGEVWKGSSFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QEELNSLLHFPPHQI QGDQFHHLYYL
26671	57039	A	26823	105	417	LCLGEVWKGSSFLTGTGRPGVF LSLHKKACYHHNHRYHHHH HHQTKP*QEELNCENMPQYNF QNGSQSYQTLLL/SLSTKFM*YS KFFVVISVMFIASSPETDF



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26656	57024	A	26807	2125	2435	VSPRQKSARPDLT*IRTLLCKVL GVLFVAGGKKGPTCILQILKG QRRQEA*CISVMAERVWASGQ A*WEVWLHWAKSIDWFLFWK QHVHALRVRLDTCLFSLEEGSS FWNQGLTWKVVRRTFSESINH TPRITLGPVYSVHGIQLPGLLN GEFKVCFVLSPRIFNLTHENFLS SEGPERRGLLGATFNCLNKRLA KYRMRNVHPKPKLVRYLHSRL PPEPAAAP*AWCGPRHLSRRQM SSSSQIGNDSFQLQVTPVHLLPL SHTTRKNPEMYDLPLLIFNPQES AILQLFHQDGECLHCSPIVGDW CHLGHSQACPSFHVPSGLFVPS LLCGAAFGRLVANVLKRYSV VRVCAHVHVCAVRVYACVC VRMTISLTVILIESTNEITYGLPI MVTLMVSTLPPGPCQAQGHVR PTGPIFRSLLEWETEVEDK*G HDFAHVLVSECISSEA*GMLLL GGGPDRSLFSTFRAVWSLSRLL DSVIAAGKQ*A*RT*SVGYSLL CPDLKGDPSAVFILRTTVHHAF PVVTENRGNEKEFMKGNQLISN NIKFKVKKTA*EERQVRDKRSR LTRLSALPIRNMCDHEIASEEP EKEDLLQQMLERR*EPGGAPTA RRATQRWGEPLAQML*LTFHG LILRSQVLTLVRGVCYSESQS VSLSEAEISQARPDEARGVGRC RRADLTLLNPRMIVVRRAPAC
26657	57025	A	26808	24	369	
26658	57026	A	26809	4	371	
26659	57027	A	26810	82	703	
26660	57028	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGGR RTQQAAGLGAPASDLWWLWLS WCLQKNMSQGGENLPAGPGSC CGREAQEGAGTSLEDAPFFEAQ LLQLH
26662	57030	A	26814	1	488	VARLYWKRPSLHACHFRDPRA GLSENPRLLQCSPSSSSGNVWG PHLYAVPCL*NGRIIPSPWNYRS LNSTTSSTCSSFAVSSPSCPWW QLPGSCLLSRSLQVAVWSQAP VPMRSEQDQLQKPPPSAGLPA SVHANL*PGDRKGSVWTPAGV AQIPSPWP
26663	57031	B	26815	51	90	

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26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLARQVSRLESGQRKYP GCRLYASCELLLCPVNPQHFAH GYVDKI\PGY\ PAGAGTLTGLHP MQVCRRCRRQAPCMKSNNALIV ILGTVTLDAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYA LMQFLCAPVLGALSDFRGRRPV LLASLLGATIDYAIMATTVPVLW
26650	57018	B	26801	1	1531	
26651	57019	A	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFHTGLAYPE HHPCI
26653	57021	A	26804	2381	3641	
26654	57022	A	26805	1	2367	
26655	57023	A	26806	1	488	MDLLYMAAAVMMGLAAIGAA IGIGILGGKFLEGAARQPDILPL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVII EQAN KRRSQILDEAKA*GRQEPLVQV FLESARKR

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26633	57001	A	26784	1	224	SRAGYDHVVEPVERGTSGVRW YACCGLMVCPANPQHFAHGY/ VGKIPGYPARAGTLTGLHPMQ VCRRCRCPVYEI
26634	57002	A	26785	112	254	
26635	57003	C	26786	1	567	
26636	57004	C	26787	1	543	
26637	57005	A	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK IPGYPGR\GTLTGLHPMQVCRC RRQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDFRFRPVLLASLLG ATIDYAIMATTPLVLIWYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIHLLCSSTGYPR AGTLTGLHPMQVCRCRR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPDPYS GAFLASCAPLGQRSQRKEQ AAIFAVLQLLLVIPIGVGGTQT NRVWSGFANHGNGPYPRAG TLTGLHPMQVCRCRR*PPYRVI PQCGTPLGQQQPEVFKQFWIL GLRLGETPHRGHQILIQGHSC
26641	57009	C	26792	1	531	
26642	57010	A	26793	216	519	QRESTIPSRPVERSNLGVRLYAC CGLLLCPAYRQHFARGYVDKIP GYPRAGTLTGLHPMQVCRCR R*PDRRGTERVSARKHVCFVVV SLFVAACRPPLRA
26643	57011	C	26794	1	606	
26644	57012	C	26795	1	1059	
26645	57013	A	26796	1	3285	
26646	57014	C	26797	1	1390	
26647	57015	A	26798	211	679	RIFKCKADLLLYDMLVYVTLWI HRAVTYTHRVPNHSYRRSNIKS ETTVPTRIVGPVERSNLGVRLY ACCGLLLCPAYPQHFAHGYVD KIPGYPRAGTLTGLHPMQVCRC RR*PKPAPLPQSPQHLCSHQPH LAQRKTGQCFLQGHCFPEKNW GTV
26648	57016	C	26799	1	774	

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26626	56994	A	26777	1	2547	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSLDLQRDLDSHTL! MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSKEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIREELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDKGDITDPTEIQT TIREYYKHLIYANKLENLEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGLT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIIIPKPRDT TKKENFRPISLMNIDTKILNKIL ANRIQQHIKKLIHHDQVGFIG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDNIQQPFML KTLNKLIGDGYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLAIRAIQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVGRINIMK
26627	56995	A	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA VPVSTLAVVLGLKTL SLLFSHSF PGRHSWALRAISLLPSFLYTSSL MNSFSYTVHLYLGGLRLCGSR DPHACGFPEGSPLPSGSAA*PFI WGMRKPSCVLAPSCSRDSFG CLSFSGHQCLHKSHVGSPPGPQ ERLYNG
26628	56996	A	26779	354	685	YRGYLRGECFP*KALCCEPAAY LQTCPNPFSGPACSGHALHSLN VGDCVYLICPRYPPLRRAGKPR DTGIEGRTLSSGGPSVHSSFHSA VLFPYTSKLLWIERRRPAGQS
26629	56997	C	26780	1	867	
26630	56998	A	26781	139	513	
26631	56999	C	26782	1	948	
26632	57000	A	26783	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCRR*PYSRGT

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26616	56984	A	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS LTPEITAELGLERLNPRRCSSCL LGLKFEYHNSNLPLQLHGQAC GDPTNSVQRAAESASRPHGFGQ PPKAPARPGWLTGKFPASVPSA SRRAPPAAVTSARHYLYRQPPP RPSSCPECNTIRLWPAFQLTPLC QGPAASERDRRKPKQRR
26617	56985	A	26768	1	858	
26618	56986	A	26769	10	1332	
26619	56987	A	26770	1	1086	
26620	56988	A	26771	1	1392	
26621	56989	A	26772	1	987	
26622	56990	A	26773	1	336	
26623	56991	A	26774	46	302	APGAVKKTWFGKKGREREKQE RR*RQLGKENENIVALQLRTD QEYWRHHSWHFFLSAAACQPE LFLKHTAKNNRRIRVSQKWK
26624	56992	A	26775	1	1839	
26625	56993	A	26776	284	816	APGAVKKTWFGKKGRERGETR EKNNQPTVRTNSQTRDTFFKT* DLF*RMPSWELPSPASS*ASKTI KYLGIQLTRDVKDLFKEKYKTL LNKIKEDTNKWKNI PCSRIGIINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPEEAAEQILPN SQSCYLILPLEASSQRGSWLY

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26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR RGVGAARGRAG/PGGT/EGGG GPESLSGGSGVGDSSGGCAPGP SAPPARRRVPLAMGPRNLLIDW IWIMDTTLGLGTEGGGHSPVL PLCASVSLLGGLTFGYELAVISG ALLPLQLDFGLSCLEQEFLVGS LLLGALLASLVGGFLIDCYGRK QAILGSNLVLLAGSLTLGLAGS LAWLVLGRAVVGFALSSMA CCIVVSELVGPQRQGVLSLYE AGITVGILLSYALNYALAGTPW GWRHMFGWATAPAVLQSLSL FLPAGTDETATHKDLIPLQGE APKLGPRPRYSFLDLFRARDN MRGRTTVGLGLVLFQQLTGQP NVLCYASTIFSSVGFHGGSSAV LASVGLGAVKVAATLTAMGLV DRAGRALLLAGCALMALSVS GIGLVSAVPMDSGPSCLA VPN ATGQTGLPGDSGLLQDSSLPIPI RTNEDQREPILSTAKKTKPHPRS GDPSAPPRLALSSALPGPPLPAR GHALLRWTALLCLMVVSAFS FGFGPVTWLVLSEIYPVEIRGRA FAFCNSFNWAANLFISLSFLDLI GTIGLSWTFLLYGLTAVLGLGFI YLFVPETKGQSLAEIDQQFQKR RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	A	26765	201	632	NLLLCPLSAESRPEEGVRLFCSQ FRSRQRPQAHKSAWGTTALSES MNCFASFGASISSADQEQHL PGAVGSGRPGEC LGPSGRCSK* GATFPGQKGRWKEARSPVPAP AAGLQSRAGHPRGGIRPGRPHG ERDSAACWGR
26615	56983	A	26766	197	777	LPSRGAGLRTCSPCLSLPPTPW TPVRPEPPQRAPPTPRRPVPST TQGLRNASARRGTGR/PAPP/VS PGAGSTR/EASWAPESAARAGL WGPSNSVQRAAESARPHGFG QPPKAPARPGWLTGKFPASVPS ASRRAPPAAVTSARHYLRQPP PRPSSCPECNKIRLWPAFQLTPL CQGPAASERDRRKPKQKRR

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26607	56975	A	26758	1	500	
26608	56976	B	26759	19	148	
26609	56977	A	26760	184	539	LPAKEEEGHSSKSGPLLGPARRA LPGTALGARGAEQGDPEADH* GADTTKRCPGLGPAPVPRKGIP AEGPRRGSRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF
26610	56978	A	26761	1	441	DENRELLG\ELDGIDVLLQQLSV FKRHNPSTAEQEMMENLFDL CSCLMLSSNRERFLKGEGQLM NLMLREKKISRSSAL\KVL\DH MIGPEGTDNCH*VCLTFLALR\T IFPLFMKSPRKIKKVGTTTEKEHE EQCCSILASLLRN
26611	56979	A	26762	1	2403	
26612	56980	A	26763	17	751	AKMPFDANKLYCSEVLAILFFS PLENRELLGELDGIDVLVFA*Q VFKRHNPSTAEQEMMENLFD SLCSCLMLSSNRERFLKGEGLO LTLL*LSHSSDSCEMPTWRGGS MEQGGRMGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSALKVLDHAMIGPE GTDNCHKFVDILGLRTIFPLFM KSPRKIKKVGTTLPPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

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26601	56969	A	26751	63	398	TPLRQPCSI RN VQQEPVGRFSGT GLPLSVARSSPWEA WPQCKWR FQNAGD*DIRQPDRGQGPRPAE PEKREPYLRSQQGAFLGSHSSGI QSQLLGLGESCSYGATGKPVHP
26602	56970	A	26752	3	231	SVHEEEKMALPLGQSHCGLLY LYY**RCFKCYSFYCILFIKNAFI Y*NI*YINTHTHTHTHTHIYIYI YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKQN TTASGCELMHTEMQALRADW KWEDSVFQTQSCLENLVSQM ALSEQEFSGQVAQLEQALEQFS ALLKTWAQQLTLLEGKNTDEEI VECWHKGQVSWLPV*KAEPRT EDLKSQNLNLCRFSRDLSTYSG KVSGLIKEYNW*A*TLLKGCQN KEQILQQRFRKA FRDFQQWL NAKITTA KC F DIPQNI SEVSTSL QKIQVRVLSI
26604	56972	A	26754	3	556	
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA EIHNKTYRHGEKLIITCHEGFKI RYPDLHNMVSLCRDDGTWNN LPICQGCLRPLASSNGYVNIYEL QTSFPVGTVISYRCFPGFKLDGS AYLECLQNLIWRPAHPGALLW KEEDLNIFSLSFISHTSGWQLLC FIFALC*SPLPPQHLVPVQLAPPH LCSKCCSPA IKDV
26606	56974	A	26756	3	1393	CLRPLASSNGYVNISELQTSFPV GTVISYRCFPGFKLDGSAYLEC LQNLIWSSSPRCLALEVKIPVS GAVRVITL PVT LGHPNVVTQR WKAGASDKGELVVLKLLFSPT AQVCPLPPMVSHGDFVCHPRPC ERYNHGTVVEFYCDPGYSLTSD YKYITCQYGEWFPSYQVYCIKS EQTWPSTHETLLTTWKIVAFTA TSVLLVLLLVLARMFQTKFKA HFPPRGPPRSSSDPDFVVVDG VPVMLPSYDEAVSGGLSALGP GYMASVGQGCPLPVDDHSPPA YPGSGD TDTGPGES*TCDSVSG SELLQRLYSPPRCQESTHPASD NPDIIASTAEVASTNP GIDIAD VDSSNIKLPDWQTKYRVASPAR STCEDRSGAPVGTHESLFFSIPS SARQDWAPLDSQLESPQCRLPT LQRDFLVD PQAERP VPLDPELT EIWCPNKNRJRHEHMSGIEA



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26585	56953	A	26735	380	731	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQT\TSPRNISPILNQEL ATSTRNLATRPRNACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLLG LTAED
26586	56954	A	26736	2	182	
26587	56955	A	26737	2	89	
26588	56956	A	26738	2	89	
26589	56957	A	26739	161	460	KMKEFMKKSSRTKDTRQQEQV LEPLFTIAKTWNQPKCPSTID*I KKMWYIYTMEYYAAIKRNNKIV FFAGTWMQLEAIIILSKLIQEQT KHHMFSLIRGR
26590	56958	A	26740	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDYFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEYYAVTRRNKIVSFA ET*MELEVIIIVSKLTQEQTCKHC MFSLTSGS
26591	56959	A	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGLG TWMELEAIIILSKLTQEQTCKHH MFSL*SGS
26593	56961	A	26743	527	825	QPLWGQLH*EVPSCWRFS*IC YSSGLTVMLSSWDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIIILSKPTREQT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSTLGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	A	26745	3	359	HRPGIPGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSHWAKSSCHCRFES RPFFLPSPSWSYNRSWGGESAE RTWMKQRGTCLSHSPDLLHP GLCQHKVGAR
26596	56964	C	26746	127	216	
26597	56965	A	26747	135	197	
26598	56966	A	26748	84	202	VLIHIRRDIMIPETVD*WEY**P* RLVPGQVQWVKPAIP
26599	56967	A	26749	483	669	
26600	56968	A	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVSRLKGVNKRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKKLMPKTEQGQKN SIR

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26567	56935	A	26717	2	237	SVRQTTATSPA HKNSKRLIRSC QGF/HPEPPPTGACYKCPQPRIP HEPCPI/S/SQDPTENWTVQLTW QPLPELELWPKAV
26568	56936	A	26718	1	313	MESAQKEAVEIFGQPHAASSSG DVKPLL FIDFYKCSGEKVVCME HALRACYMCRKSGHWAKECP QPGIPPKLCPI\GDPTGNQTVQ LTWQPLPELELWPKAL
26569	56937	A	26719	377	583	
26570	56938	A	26720	1221	1394	VASFYSLLQPPYPSTSFQSWR HTSISPF S*FQFLSFSGIFWQPLP EPELELWPKAL
26571	56939	A	26721	160	234	
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHFLLSILAS PFNL SLLLISVPFLFW*RTETRFI WQPLSEPELELWPKAL
26574	56942	A	26724	809	874	
26575	56943	A	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQTTSRPNISPILNPEL ATSARNLATRPRNACSPGFLLS RVPSVRDPTGNRTFQLTWQPL PEPELELWPKAL
26577	56945	A	26727	1	1011	CSEYEDSSPAPVPATDLSTLSS SVPQPQDTGTSQQHLPLDPWHE LLRAQELQGATNHKGYSIAEH EHAGLG VQGGNGALAFSNSGH RHAVPTISSGTGRRRTSPSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTTSRPNISPISNPRQRQV LSMDPKLRHRSRTGKAAPWC LIIAGTPL
26578	56946	A	26728	150	211	
26579	56947	A	26729	445	549	
26580	56948	A	26730	193	249	
26581	56949	A	26731	372	564	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQTTSRPNISPILN/PEK KETRFIRGPKTPAPVMD
26582	56950	C	26732	185	640	
26583	56951	A	26733	1662	1774	
26584	56952	A	26734	233	527	

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26560	56928	A	26710	241	957	KSPQIGLQGSWGAVGVGM RDP KERATEASKPDLLAQRQEGHI FILFFSDYIPIFSSYLSLQRSSRGP SFFGPFSSPHNIPCEGRQNSSETPP WPSLGKRSKKSSLYPLPKAPQP KSRAPSPISNNLKNFPQPSEK KD GPQPLWPQKWPLAPLFSRSPS* DDSGPCTEYCRARRRFSKFEDM AHIGPPKKVLYKIALGKFWELA DAKKKRKKG TSETETCLLSRAT ELLPKGKRHC RGIL
26561	56929	A	26711	496	708	GMLFRGSGACRRGGRTGGSGH A*PEPPVLPPLLHAPEPLNSMPH GLPAPPASPC HFPNLDSCVHSHS DTPLSVLPLPHLKSP LSSSDFC S YEVKKDAILSPMLSWWAGHRS AAGED
26562	56930	A	26712	302	561	TFLLQLAAVWSADRVREALRP ALWDWRS AVPHPS PQGTG*R GVGVHPAAASRG GESSHPTAF DRSPPPPKPLRI*PEPSARSGLP
26563	56931	A	26713	1	411	LLVFQVHQCLHCKLL*/PSYVPL GYTEAFLATQ NIGRVSLWAKH GHPDPFPLARAD FRAQESPSPN DPSWLL*YFER*WSQATT KG*N RCC*RCD*LQAPSRRPEAVHTN DPR*REVREEH MV LQVLTR
26564	56932	C	26714	361	642	
26565	56933	A	26715	1805	2260	
26566	56934	A	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT TPATRAAFLAASCGPLHSCPTL LCSQLCCFSR SRSRVSGPKASLG IKEIASVDRVNTRRPACSTSSWL HNSGFTLSLANRDGGKRIRSET AKKGMSGDRSMKSWEVRRGY RWSSRAVRRPRACSSDGGTHF ALPMAARGSSGSPSGSPAN SVR QSLKSESSISAIWVAEQ AAGNV PRTSAQFGTGSE SNTAARLIE KLLRAELDKPEIRDERIVGWWT TFGRPQLGSRVGF CACSLAARM SSTSQNLEAAFGGKFCFLWALL LGLDDTFESRISDTGSAGLMLV EFFAPW*VHSESANTAARLIEK LLTAELDKPEIRDERIVGWWTT FGRPQLGSRVGF CACSLAARMS STSQNLEAAFGGKFCFLWALL GL

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26548	56916	A	26697	1	179	MWKGPKGLDMYGKSSVSPKTS DILGRD/NSPAGLEGANSQVAN CLWRGPCGRKLWEASRN
26549	56917	A	26698	2	140	DN*KGVHKRILSKLAPELGSFK GFRSLAVNTHNSYGGKGNRPL KIR
26550	56918	A	26699	3	601	
26551	56919	A	26700	232	1809	
26552	56920	A	26701	1	851	MQQEDPEESTKSPNPTTNKKQE KKLSLFGGLFTWTRVKFGAVT QIGGPPLGDQSPVLLLLQRLFSK GYRVSPSKAQISSPSVTYLSVS LIKTLTKTTLLPKEAGVIHCKG HQAASDPIALGNTSADKGLFRP PPFSPHQARGFAPAQDWQIDFT QH/RP/GVRKQKYLLV*VDTFT G*VKAFPTRSEKATAVISSLLSD IIPRFGPLTSIQSNSRLAFISQISQ AFFQALSIQ*NLYIPYSPQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPLALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLWVVDFTFG* VEVFPTGSEKVTAVISSLLSDIIL RFGLPTSI*SDSRPATKSSFSLSIP TLGSHDAPNPTRSSPEKHRPLSL HTIPQNFRCPTDLPFRFIFFAFF SNTLHIMGKMAAEGPKSTLYC QFTEK
26554	56922	A	26703	96	415	
26555	56923	B	26704	1	933	
26556	56924	A	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH YHHRHHHRHHHYQR*K*NPGL PLFVYCYFQNH*ACHCSWGNS EHMTIASESA VPLQPPQDSQG FFEDLELHYFFGDPSETRPGKQP KVS VQQIL
26557	56925	A	26706	355	1014	RHLRPQERAPAPSGSVPSRPGCS QAPGGLLRVGRGGMLLPGCAA VADLQEEVPGFSWDAWAVKG EQRQGGGGVVKH*DAIPQQRV SDPGPPEPLASAPGQLSPSTPEY RRPPGESRRHRRPDLAQDQGA AVLLLAGARGLSPLPRIPALGA ASFPPTLQFFLQLPSSGASTTSA GFFLLVLHQPLWLLLLDFLFDN LLLLRHSLFIPHGFLKCVSIPAF
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWP VFATWPVWQDMWPQQA WPLP QGVDIP*ACPPPLRT*WL*ENR KAGS
26559	56927	A	26709	110	195	

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26538	56906	A	26687	120	594	
26539	56907	A	26688	117	487	
26540	56908	A	26689	2	2482	
26541	56909	A	26690	2	654	KGDVGEWLSAGKGESSAMFAS EQEISKDEQGTPVLGSFYWEVD SPRKESSQAWAPGQEWIKLERD TTECKMFEQLKPIEPVQKTLPW VGEVAATLQEAMKRDCWREA RVKKKPVT FEDVAVNFTQEEW DCLDASQRVLYQDVMSETFKN LTSVAWVRKKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEKRRKRKRERK KKKKKKKERTTTLWGNPLT
26542	56910	A	26691	789	1072	
26543	56911	A	26692	1246	2367	
26544	56912	A	26693	579	1214	
26545	56913	A	26694	119	1870	SCSRNRLPPVSESLTRPLPSLA RWLPPGLRQPSSRDYWPKGRL RLSAVPSPASPWALVSCLLPSS SQEKAGKILKKRVEKQQPEEKV GKGLEESLCPSSMSNHTKERV TMTKVTLENFYSLNIAQHEERE MR*RILFEKIEEEGLKDEEVINIG NVFLRKETEFRLRLKRTLGLD FESLKVIGRGAFGEVKITATCQ VGHVYAMKILRKADMLEKEQ VKHSCSSAFILVEADSLWVVK MFYSFQDKLNLYLIMEFLPGGN YLTMKGHKDTLTEEETQFYIAE TVLAIDSIHQLGFIHRDIKPDNL LLDSKVLGGHWHELFPQEPRLR GFLSQCCDTPFRALRFLASPSFQ VPLHSPRDLCTGLKKAHRTEF YRNLNHSLSDFSKW*QLR*PK AETWKRNRRLVSNICGF*KN AENVSLGQVRWLTPVIPYIAPE VFMQTGYNKLCDWWSLGVIM YEMLIKHLHGFRGLPQETYKK VMNWKETLTFFPEVPPISEKAKD LILRY*RTSLHLQIKSDDTSNFD EPESDILKPTGNTTSIVSCDYK NKDWVFINYTYKRFEGLTARG
26546	56914	A	26695	271	446	YLVHILDALPRDPTALRRRQRC LGS*RKHQTRLRSGRPSSGPGG TDISVTAVSAPAQK
26547	56915	A	26696	1	171	WGVIWRENGRCFSGLLRAGLG AAWEPRVGEIKILVS*LGTC*IK LICQSWVGANPRA

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26526	56894	A	26675	1	1364	MEMIWPSKGMPTSTSYSNKES SLLSVVQTSSYSHTHTRGSSEE VESLNRPTGSEIVAIINSLPTKK SPGPDGFTAIFYQRYKEELRIK YLG IQLTRDVKDLFKENYK PPL NEIKEDTKK WKNIPCSWVGRIN IVKMAILPKIIVEDALQIYYDMV LVCVGVGVSCRIVISSLEVLESR RGQRIFFLVQAEQVLWAFKEVS SNCNDKSTLRGSVVKLQCTSGT SAFDIFQVGSRLGEHRLPSVH SATYMSLT YFELAGLLEKSSQL VGSTGVEDIVAIMIPEPKGKEIV SLLERNITVTMYITIGTRNLQKY ERWKKKRTK GLEYQEF GDDV KFRSLDIEAEMPD LHLPRNM HASSPSKRTARGRNKNKSSRLT MFGVEIQEEEEEEEEEEKKKR RKEEEEEEEEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRGRRRRRKH
26527	56895	B	26676	1	499	
26528	56896	A	26677	1	1684	
26529	56897	A	26678	2	297	
26530	56898	A	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE EEEERRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRRR RRSHTSIPKESTLLQSQSVGLG
26531	56899	A	26680	1	1617	
26532	56900	A	26681	92	338	LEKEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEN*NVERY KKEGQW*KQRRQEKGLILPDG
26533	56901	A	26682	1	548	MVDQRHLVLTSSTKKNQNNNF QVFVIENVGREPQTDKIASPGA GQSCTASVTADLLSRDLHFTKV PSWSSDGPPYYPACHLMSEPY FWGSCCYDTPIKTKTNEEEEG EGEEEEEEEEEEDEEEEEKEE EEEEEEEGEGEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RKPRGGR
26534	56902	A	26683	1	1215	
26535	56903	A	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPPSSSIPSR LPSVVL SVRILS LWILACLAPWRWDL LRKASCL PAFSLLSGANGSFSLGFQALL GRKEEEEEEEEE*EKEKEKEKKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKNF
26537	56905	A	26686	24	355	

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26515	56883	A	26664	3	276	IKSIDDTSNFDEFESDILKPTVL SSAP*AVHWRQGSESTLTSISFP VATSNHPETDYKNKDWVFINY TYKRFEGLTARGAIPSYMKAA K
26516	56884	A	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEEEEE/ ERRRRRRRRRRRRRRRRRRRK KREKKKSWVDCTEEVAKYVGL ASLRISRVPPTDSTKEKTIEKVN RRK
26518	56886	A	26667	1	370	MHVAWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGKKNIRAG EWDELKYDRFPGQPKKKKRRK RKEEEEEEEEEEE\KKKKKK KKKKKKKKRRRRRRGRRRMQ QSHPNPTSAILAPWA
26519	56887	A	26668	1	430	MTFFPFDKRETDILLINFSMEH CTRGQDPLGYQTTKKGFKDTE TPEKESLESKAELGRRRKKKN KEEKEEKEKEKEKEKEKEK KRKKKRKKKKKKKKKKKKKK KKKKKKKKKEEEEEEE\GMRKR RRRRRRRRRRRRRR*RRRRR RRRRRRRRRRRRGRRRGRRRR RRRRRRRRRRRRRRRRRRRR RRRRMRKRRRRRRRRRRRRRR
26520	56888	A	26669	1	708	
26521	56889	A	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAAVMFFCSVLGKFQMN EEEVEKRRRKKKDKKKEKEE EEK/DERRRRRRRRRRRRRRR RRRRRRRRRRRRREEEEEEGEE EEEEEEKKKKRRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRHWDRLEGGGWRR VRVEKRLFRDYPSSHPRGAFA TSPDSIGRCTLRFPLQMGHLHQ PALIAILRSGADLSHLEGPMLEA GASACAPAVSPGDQALQQHPG EGRKVPGRKKKKKEEEEEEEEE KRKKKKKKKEEEEEEEEEEE\ KKKRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRNKQTKGP PCKNLMLVFCPQNKAPSPCLQI AAEFSSAWAR
26524	56892	A	26673	365	670	
26525	56893	A	26674	29	370	

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26509	56877	A	26658	1	2267	MKVELMGFAEGLAVRVREQEE VRLNWKVELLWTDLRDVPKG ANSFRVSGSSGVEVFMVYNRT RVKEPIGKARWPLDTDADMVV SVGTASKELKDFKVRVSYFGEQ EDQALGRSVLYLTGVDISLEVD TGRTGKVKRSQGDKKTWRWG PEGYGAILLVNCDRDNRSAEP DLTHSWLMSLADLQDMSPMLL SCNGPDKLFDSHKLVLNVPFSD SKRVRVFCARGPEDVCEAYRH VLGQNKVSYEVPRLHGDEERFF VEGLSFPDAGFTGLISFHVTLTD DSNEDFSASPIFTDTVVFRVAP WIMTPSTLPPLEVYVCRVRNNT CFVDAVAELARKAGCKLTICPQ AENRNDRWIQDEMELGYVQAP HKTLPVVFDSPRNGELQDFPYK RILGPDFGYVTREPRDRSVSGL DSFGNLEVSPPVANGKEYPLG RILIGGNLPGSSGRRVTQVVRD FLHAQKVQPPVELFVDWLAVG HVDEFLSFVPAPDGKGFRMLLA SPGACFKLFQEKQKCGHGRAL LFQGVVDDEQVKTISINQVLSN KDLINYNKFVQSCIDWNREVVK RELGLAECIDIIPQLFKTERKK ATAFFPDLVNMLVLGKHLGIPK PFGPIINGCCCLEEKVRSLEPL GLHCTFIDDFTPYHMLHGEAYS LECRQHWGKNLYFRVGLKKK KKKKKKEKEEGQEEEEEEEEEE
26510	56878	A	26659	1	990	
26511	56879	A	26660	1	235	MTAKCVCGWGVGEREREKER EEEEEEEEEEEE/ERRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRKI
26512	56880	A	26661	1	1101	
26513	56881	A	26662	348	806	
26514	56882	A	26663	39	684	LRCENPISSHVGHVGVSLAHTR GLFSRLILADREDISENWCSLVC CVCVCVCVCVWWLCISLFPGD MMTLLMKKDTLTEEETQFYIS ETVLAIDSIHQLGFIHRDIKPDN LLLDSKGHVKLSDFGLCTGLKK AHRTEFYRNLNHSPLPSDFTFQN MNSKRKAETWKRNRRLAFST VGTPDYIAPEVFMQTGYNKLC DWWSLGVIMYEMLIGKLHG



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26506	56874	A	26655	1	1167	MAPRPQAARLPSCGTRSQGAA RPPPLGTAAAYRPLSSRLTGPP PASSWLAIHFIRIVGSSGQGN QRIKYLGIQLTRDVKDLFKENY KRLLNEIKEDTNKWKNIPCSWV GRISIVKMAILPKVQAILMLVLF LHLFCKYNIVGMENAGNGHD WSLDRHLMQASANQQATQLAI SRPSNQSKAQDFLRLLRKEKQT ALDTFAPLKEQAQKWNEGIR SSVIPGIQHQSLLAVLTFNSSK TSLGDRARPVSKKKKEESRKK KKKKKKKKKKKKKKKKKKKK RKRNNKKKKNNKKNNKKNNKEN KKKNKKKKEKKKKERKKKKR KR/MEEEEEEDEEEEAEEKE RKERKRKKEKGRREGKRKEGKR EGKGRRGRGRRKNKEERRRSR
26507	56875	A	26656	342	616	RILHKSFRKLLCKGSFCSTRSPT REIRSKKKEEEEEEEEEE/ERR RRRRRRRRRRRRRRRKKRKRK RKRKKKTKTTKKKKKKKKK KKKK
26508	56876	A	26657	1	705	

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26488	56856	A	26637	1	290	MKKKKEGRRRKKEEGEEEGEE E/DRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRTTT TTTTTTT
26489	56857	A	26638	2	423	
26490	56858	A	26639	3	167	QKKEDEEKEKEEEKEEEDEEEE /ERRRRRERRRRRRRRRRRRRR RRRRRETQEAETI
26491	56859	A	26640	1	325	MEKNEKEQEEEEKKEKNSKKK EEEEEEGGGEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRGRRRRKKKKK
26492	56860	A	26641	1	618	
26493	56861	A	26642	1	291	
26494	56862	A	26643	3	155	YRHLPKKKEEKEEEKEEEEE EEEEEEEE/ERRRRRRRRRRRR KYEKKCL
26495	56863	A	26644	1	1410	
26496	56864	A	26645	578	842	TQEAELAVSRDHATALQPGQQ SKTPSEEEERRKKEKEEERRR KKKKEEEEG/MKKEEGRRRRR RRRRRRRRRRRRRRRRRRRR KKKEEEEE
26497	56865	A	26646	215	471	
26498	56866	A	26647	432	761	
26499	56867	A	26648	1	357	
26500	56868	A	26649	2	281	
26501	56869	A	26650	533	758	EQKKKKKEKKKKEKEKEKEE EEEE\ERRRRRKRRTRRRRRR RRRRRRRRRRRRRRRRRRRR RRRRRNTEK
26502	56870	A	26651	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEETLFSNM
26503	56871	A	26652	1	279	
26504	56872	A	26653	1	795	
26505	56873	A	26654	1	642	MKKCKTSVIGIATFYLSIPHIYT PPNQTSFMAAIAIEVQLTSAE PASIGFPVQKSPCGHLQLNGYK SSSKQGFPPLLQESWNSSVKI TTCNVGDKKNINDRRSANMMH VNNFPFRRHSWICLDRVQSETL PQEKKEEEERRRRRRKKKEE ERRRRRKKKKKEEEEEEEEE/ RRGRRRRRRRRRRRRRRRRR RRRRRRRRRRRKKERISL

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26477	56845	A	26626	70	551	AAEDVWVYPSELYWPGPHGHC ETPRAGVFVVTSHHEGPGAGTA SSSSKGPSWARWGLEVSPLRWP SGQVGGAGSAESGQPLGSGFTF KAMGNLGESRARQAQLIHDRN TASHTAAAARTQAPPTPKVQ MTWTREKLIAEKYRSRDTSLSG FKDLFSMKP*VSPLRWPSGQVG GAGSAESGQPLGSGFTFKAMG NLGESRARQAQLIHDRNTASHT AAAARTQAPPTPKVQMTWTR EKLIAEKYRSRDTSLSGFKDLFS MKP
26478	56846	A	26627	479	961	PQSSLQGNLQMPWGSCLDST HYRPSLVGVDFQLPSFWLVICG TCKHCHRMLHSVALFWVPLHC GWSIPRPRCPHPHPPLRGPS HPPSPWACPPRTGVQSATCPF A*RPTWSFTCDPTTKRSMRGLT HILRSGEKRPLPALCARSTSGSA TTSPGT
26479	56847	A	26628	1	223	MGAVQKAYNLQKKRRRRRGR RGRIRGRRGRGRRRRRGRRRRK KKKKEEEEEEEEEEEEEEEEEE EEEEEEEE*VEEEEEEEEEEE EEERRRRKKKKKKKKKKKKK KKRKKKKRKKKKKKKE
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRRKK KKKGEERRRKEKKGEERRRRR RRRRRRRRRRRRRRRRRRRG RGRGRGRRRRRRRRRRRRRR RRRRRRRRRR
26482	56850	A	26631	1	327	
26483	56851	A	26632	41	246	
26484	56852	A	26633	1	170	RKRRKRKKRKKKKKKKKKKKE KEKEKEK\RRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRNTNNETGE
26485	56853	A	26634	1	282	MCIESEEEEEEEEEEEEEEEE EEEERRRGRGRRRRKKKKRKKK KKEEEEEERRRKKRKKKKEEEE EEEEERR\MRKKKKKKKKRKKK KKKKRQSL
26486	56854	A	26635	1	396	
26487	56855	A	26636	1	255	MLWLPQPALGTRAAETLACSR RRRRQLYNCCYLRRRKKEEE KEKEEEKGKEKEKEKKEE\KRR RRRRRRRRRRRRRRRRRRRRR RRRN

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26464	56832	A	26613	576	927	FAERTRTHH*PKPRWKGALGC RARTAVTSRGCLAPSRRRRLP GRRASQPGPNADPKACRPWN PRGSQVHAKRNALCFSRASDAP PRPDASPGQIFPGRRRKECQTC KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFQVWKIDASPGS PIPLNAP*PSPSVQTTPTTGH RALSTVSEVPGAGARLTYRVPF TRCKRSLILPSPVWVSRIPSTAK SPILISSPGGAHAASVSALTLS GYE
26466	56834	A	26615	87	347	GIRY*LCHGFYHAYLGFRRTS SPLQVSRPPPRGTQSEP*AQSP RSPELELGLHTASHSRAANAAS SFHLRFGFPGFHRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSPDAYDLVFL LARE*HWKH*TQSILTIAQCVF PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCAALGQ*KCKMI QLLWKMV*SFSTKLNILLPNNP AVVLLGIHLKELKTYVLTETCT LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIAASRSVRRCYQS RPGLLPTAGHHPQFHLYSDCHG NDIYSVYYQCEHGHAASSSETG VPRFPCPWWSETAQ*TGCASHP GPSAQRSAL
26470	56838	A	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE QASWARNLSRFLLGMATVSG RGLPSGPGPRAMSPAGEPAPGA AEPAPPGSAAIPHRRPLLQ
26471	56839	A	26620	723	1023	ITLLGLSLIPLISRLPWTQSWG PLSFLSTPTSLISSTPLILNTIN SLMTLRFLLPPGGAFF*TPEPCI PTQHPLDVDSLTGISNLPRPQSC FHCLHLS
26472	56840	A	26621	99	288	CLCQNKLGEGRDDNFTSWQSS AC*TFCFLLAVDSAETTAES*C CCCCCCCCSAAGGWRLVH
26473	56841	A	26622	130	450	RQLKLTAGCAKSPWLFWLKSY HSLYLAAACLLGLTYTRLGRSQ SSPPIHSHEFPATSL*QLHGG QPA*WLYDGPATP/SIAPPAHLLP PPWRGGTSPWLPSPSPLQE
26474	56842	C	26623	1	672	
26475	56843	A	26624	408	581	LIKDESAPRTPQTVLASAQFCLL CR*ARCCRGGScccccccccccc WWWCCCCCYFGND
26476	56844	C	26625	66	264	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26455	56823	A	26603	28	457	GGIPDSTARLSILTTPRHHLQRSC SCNGTATRFSGQSYVRYRAPAA RNWHIHFYKLTLPQAILLFTN ETASVSLKGFEGCLDAVVVNEE ALDLLAPG/NDGGRLAGDTSPH PVLPPQ*LLQPEHMPQWWEVL MDPRGRLCLQMS
26456	56824	B	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGSTHASGQL*TGDR S/GPMGPPITATQ*DGDSDAYH GLATLHALLPALPGAAGF/PSGT SEPCPSSPC\QHHHAGQLGHD LPVHCSEDPRPQPPPLGGPLEDL PSLLWHSDFFI
26458	56826	A	26606	69	551	QSGRSPQHVFPVSRGSGARSRG WILVHPSQYHHNPQRIYSACGR SGEHISPGYPCS\DGHDAYDQQ ADGTHHDACIFH\PRGSPRSP\G QCCLLTGGSRSQTSGASATPG GRRGG\PAQGGG\PASRNSSVEE LTARVLA PAPAPALASAQPTLP GFSISPSTK
26459	56827	A	26607	476	1016	CLWLLSCLYCSLGDCCLLWWAV SVLCQVSAPRQALCFAPGENGD GGQQGLRGAPPGPRGPAPQP GPGYPGARQRGSPQQP*LSSEP GPYLRLSRSGGR*GPGRCCSRSP PGR*PVQAGDEDDQDAGSHI*T QPRVSEEGGTDEDQWSLPQEV SASVPYQPLSHCQTPASLQPH CLFS
26460	56828	A	26609	247	342	RSIMPWLPKGSWEVSSIPP*RC LHQLWSTSRNMAL/HVRVLQT EQAVKEYNALVAQGVVRVGGV FHSTC*WSLKRRINH
26461	56829	A	26610	129	272	NDTVSGLGRLESPTLMRQRNV CSHCYPGSAK*GYMIYKDALPR RTSL
26462	56830	A	26611	133	453	QVDPNTVLRNAVHTNTYLQGL THPSANHKSLYTLNLFHICR LHTRRMHGKTGRVYGITQRAV GIVVNK*VTGQILAKRIVPIEHI KHTKSQ*SFL*ELRPSPVAS
26463	56831	A	26612	352	543	VPSINCGVPQGNMALMCRVLQ TEQAVKEYNALVAQGVVRVGG VFHST\SDGSLKRRINH*VPKKK

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26451	56819	A	26599	971	2485	FISSCFVRACGTLNPGVTFMFYVI LGKFCDFAEPWFPVHMQEQLR VVGKGLWGFVRVSLSGFRIHGP HQKTASLAQVHKAVLHDGRTV AVKVQHPKVRAQSSKDILLME VRALPFSFLCPQSTFMWLVEA KKNLPLELDFLNEGRNAEKVSQ MLRHFDLKVGGTMQCRVWW SGGLMEFVDGGQVNDRDYME RNKIDVNEVRSRAQGCCAGER GVNGFVHCDPHPGNVLVRKHP GTGKAEIVLLDHGLYQVEEAFV TQPWGLWGQSLIWTDMKRVK EYSQRLGAGDLYPLFACMLTA RSWDSVNRGISQAPVTATEVG GPSRPCLFLNAEISHLNHNVP MLLILKTNDLLRGIEAALGTRA SASSFLNMSRCCIRALAE*VWA PPSPLLAP*ISFSEAFNLWQINL HELILRVKGLKLADRVLALICW LFPAPLCTVHVTILLWNPLRT LWPLSQGPQAEWHSSLFFSKK TQQPTFPFLVCAIGLDVPTTSVK
26452	56820	A	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA FWEALEANTWVPCVRL*RTPV SAELLGLAPGGRWRAVNRDRG RVAAASSLGEP CYSSPADASFP RSDSGGLDRQGGSCRYPKELFG SHPQARCTEGSLQVL
26453	56821	A	26601	377	962	LFSIFITQDPKLRELLDVGNIGR LEQRMITVVLKACV**LCSI*AN ASVIYIFQEWTDHLLVL*SMC HLNLSPLLCSLHSIYRNREGGS WGRKKTIC*LRCFISQND SIPQE DFTPEMQILE*NLV*KILIAWFFI VFSGAKSKPYLTVDQMMDFIN LKQRDPRLNEILYPLKQEQVQ VLIEKYEPNNSLARK
26454	56822	A	26602	1	810	MDAKKRKLYKYASTDSPAFAI TFIIMPYMENQAAKLAFERLSL NELVFSSEALTHSETFLPQPDNR HQNMSSTIHTAPIDTALGGNPA FLYLFLQDFQPTQDNSLASVTP SAGVSARLAPPPTGPFDTV LDVLDEVGGQGEVESAAPESA GIGEEGGGGDACHGATSRAP*Q ASPPPPSSPIPADSGAADSTSP WPTSSSTRTTTSVNGPGVGGG ARRAETPAEGVTDASELSCVG

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26447	56815	A	26595	3	699	RGRSRANSPQLLLEGGADPTVG DIGHLSVGVPVHNAV GACQP DQTPPKHLADNPGPWTLDA LT YQPHAANSCHKRGIAAS*SLMII MVIIFLVLLFWENEVNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIIQVRVIREPDHTCKKEHVFI HERPRKINGICISPKKVACQNLS AIFCFQSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	A	26596	2	483	
26449	56817	A	26597	2	1041	WPQDGSCTWLAVAMGCWLAT QQGSLTRVPVATSGIQGCQAAP SPMWAAWTHGWASCYFRAAL QLPLPPGSTGNGSMSTSTAYSA SSPGFM/YTKAQGERSDHKENV FYVQHQQYVGGATQAFKEN NQKAYKETYGVSHTRHMLQ IPKQQQNEKYQVPQFDQSTIKNI ESAKGLDVWDSWPLQNADGT VAEYNGYHVVFALAGSPKDAD DTSIYMFYQKVGDN SIDSWKN AGRVFKDSDKFDANDPILKDQT QEWGSATFTSDGKIRLFYTDY SGKHYGKQSLTTA QHLQQYLT YKRSFSIVVD AIIALPPLKRAAW PKSRHPPQVGLMEVQHLFPIN NFEHV
26450	56818	A	26598	116	338	

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26436	56804	A	26583	316	723	LVGGWGGGLWGGHLHGPLYGQA QGASPLLPPPPAHRPPPHRHST EHGVEHPLVT*TAPLSPCPLGFR LGQLALHRGASTKGLLTGGVW GLHSWPIGDGRATIHEAVVRAS PWPSRLGTIHGVRGRDVGEG AELPAV
26437	56805	A	26584	177	418	RNPVVAQGLLCACRMFKVGNR TPSSSAEWSSFAPPKKGPLPKA TSEPLFPHPKRR/PLASVPSHREC RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	A	26586	1037	1455	EESYGILLSVPSVTGSLLLQDLH KLGCHQFGHKKRRVSGIWMA VLPFPFRCQPHLLLLLENPRAN GPARQPTNHQPP*KAGTQLPNS VAPVQSQTGFPTPARKARAPT WPGAARPPGTASNKSPARSPCS SPSFSILP
26440	56808	A	26587	175	450	
26441	56809	A	26588	77	337	RDHEPTRRKKVTRTHPNVRRNK LRTRRL*EL*HSLRGSAAFLKE GRPWRSGGAQRR*KYWRKG KYSGKMQSWSRVYCSLAKVRA
26442	56810	A	26589	1043	1555	ALRQGPEGARAPNMDSSVSR QVPGPQVCRAVPTEILASPAVE RAPAAALSSTTIWMPMSLCPW RPVLAACSTMTVRGRSTMYLP TTTGNAGCTWPKASLATRWLS SPMGRQARSLMLGAQVTLWD RSMPWRRRGRSSGRNLSTI*WR LDWSLRRTWRSGRAWMSGIST
26443	56811	A	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE HIRT/RRRKKLRTHLNIRRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRGRRG GRRRKRRRRRGRGRGRGRGR* KERRGREKKKEEEKRRRGRRG GRRRKRRRRRGRGRGRGRGRR RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAAFLKSVRRTTHQFR TH*FHIHKNRTFTSR*SH*RMQR WDQREVKVLFL
26446	56814	A	26594	573	968	AQRFCHSQWRCSSRAVLEENP APLDTTPLSGRSKSSGRGCLVS LGL**PPSTRSSHL*QPSP*AS TFLQVRMTAPSGL*PQRPA*KL RSSPLLLTKNPFPEAAAF*SRGP PVSLKDTASLQAAFLGWP



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26426	56794	A	26573	3	266	GNHCRRQYRDAQ*WP*EAGRY SSCAGSARLGKAKG\RGPQGV MGNE/MRSRRAQEFKKYLHSK TSR*KSHTGPEAELTSPGAKKE GCSQ
26427	56795	A	26574	36	384	GWYCSSLSDVCSGGNSSAHSQ LPHQPLPRLRPGGSCHPRESSSP SKQRGGPVGDRQRCLPVRH*RP SQTIRAEQEPRSAAPRKRRAKE GTRRSRGSSPHPEKLGDLGSGG QEVPR
26428	56796	A	26575	101	334	CSTSKEKWQCGLRAECSPVFPA TEVPEYSC*GRKPSHLSCHRAP TLEEAANRWKWPCTQYDAIQNA CYYNDSLVLRLS
26429	56797	A	26576	435	761	QGTNTWVPHWVLRLLGHTSP PEGIAELPRSLPSLTHEQACQLD CVLVAIGTAILVAQTATTSPIC GEADHPASTPLPPSWPPQGRQ LSC*NPPLGPWPSGRVQTP
26430	56798	A	26577	38	236	RLLPLENCCSSASGTCAHQAP LLLCSCPNC*SCCCHHCCCPC GCCWHCHRPSTKGNSATFTA
26431	56799	A	26578	1316	1548	FFSITGLSSVAGGQFVNLYLKR LNSNFIYLSGYVIVYINIVFIYC I*KFVLHVTLRDCKTIVKKH VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK ARDLRGKKKEELLKQLDDLKV ELSQLRVAKVTGGAASKLSKM *VRRPDHSPRGWGARVHRDRR RISKLA
26433	56801	A	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAASAGLCSNEP RFKARDLRGK\KKEELLKQLD\ DLKGGSCPQLTRSPKVTERCGP PKLSKIR\VVRKSIC/RVFSPVIYP DFRKENLQGNYSYKG\KKYKPLG PCGP*GRTRAMRPPGSNKARRE NLEGPKEAGSGKGAFTRCGK *RGSRALRGRLCQLKHKENLKT KKQQRKERLYPLRKYAVKA
26435	56803	A	26582	164	346	LHPGRRPGLTHLGVSPGPGPT EKLAPGKPSSAACAPSPPALD* HIAFGVDALCPTFGLN

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26419	56787	A	26566	525	716	PTCLLTPPSKGRQTPYATGELR LASDGCPSGTLKPEEGAGSNTQ ANRVWSGPSANSSRPAEEGPDC CRTTCRRTTCWKPTTVTTCSSST PCCQPACCVSSCCQPCCRPTCC VTSCCQPSCCSTPCCQPTCCGSS CCGQTSCGSSCGQSSSCAPVYC VSSCCQPSCC*SGPSSAGLLEFA EGPLQTLFAWVLLPAPSSGSFV PDGHPSDASRSPVA
26420	56788	A	26567	3	390	EGPCCKGWCC/RSPDTML/CPT VFITCRPGDSLRLHHQGPRFQ AQN\CQPFQQTSS*LQEFFPIQ WCLECRRALAGIWQVPLWDEA SLPEEGAGSNLCCSAASTGDTQ ANRVWNGPPANSSRPAGEEAD
26421	56789	A	26568	658	1005	NSKYWTPSGPPRLASGAIYGN SLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVG SQVQHDNELYFC/ APAGSYPLWVKALPQPPSQPFL KPVASM
26422	56790	A	26569	1149	1715	VLQLNLPGPVASWCSRVDGPPPL ARPIPPAPHTPLSSAGPSAAAP GPARQLPHPRGDSRTARLLPGQ GSS*SWR*GAWQSGCQSYRKP GLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGSGPHL GPDG*MVG VGPSGAGAAPEPA PGLWDPPGHCSQASTPPGACKE RETLPTALPRLS
26423	56791	A	26570	32	335	LWSLFDHHVQRAVCDSRAKYR EGRRPRAVKVYTINLESQYLLI QGVPAVGVMKELVERFALYGA IEQYNALDEYPARRLY*SLSY*I YELTKCKDSQEKNG
26424	56792	A	26571	407	842	TEPLITINRLQRRRRSAPVAAAG PAGTLARRAPAVTAERAAGPG PASVHRRPGWRRRAQSGPAAQ ALRPPPPR*PRDSASPLSRKELL KLLGTKHYGRLTATEAQAPQG QHKLLCRETGELVPHWAGSHY RGISNPINNIQDHIL
26425	56793	A	26572	409	614	GLPPPAVGDRQRCPLVRH*RPS QTIRAEQEPRSAAPRKRRPKEG CRRSRGSSPLADNLGDLGSGGQ GG

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26415	56783	A	26562	1	1073	MHATNSSSVPQEIQVEALCPLL TQPQKSPSITSAMLCQLKKPQPS RSKEREADPISCGPECQGNWDL CVEAATGLYGDGHLRDSSRTR VLMTTGTYRDLQGLEGRAGHV AELHVLVPVWAIQDRGYVLWC WTASLHPRDVAREQGFPNDCT WALGCTLTAESTHTHSAALAR QAYSQLSKKPTLLNEPEHITEK KFINLARFEALNSRTWLGVLY WIAIQDVPVTVESTTGQRAAR ISPREADRTL VKGQVQGIRQTVI MSVPGRKEGDKLKEVSDGREA ANQAGMKWGKECKSSSGTEN AMSGKEVGILQEEKGDWSHG VRGWQEKWMTYNFWACGRG KNATCRLEMTRTSENDLKHQ EGLWHGRERAMLGDTHTLAW REEEMEQKQALRIHSLYGKTSG QRALGSWWVERFMGMRSGSSS DCNGLVTEG*TLQSACIPEPTCS H*GSPAP*LHP*GAEKQSSTTEH SPCPGLPRQAERGAQPRVPPCP QDPADPCKFQWS
26416	56784	A	26563	1	387	MESTEIGPHIYEQFTLT K MTRKF NKEQLVLISLALLDSGHTSNL AWPSCLIVSGV GSCRWVCGLT D/CQE*SLRPSQSAGVCRRSTPD PVCLGVTRGGCRTEKIAACSFL WKLRPRGAPARCQPELSCM
26417	56785	A	26564	47	472	LLRLHFWQEERLKPSRKKITKK HTKKRTASLILHAMICCRSLNSS KTKNTKCLNSINQRLKILSLQK GDPLESTCRH*CCHVHRRTKAP GQRRVGRQHVVSAGNHRHPHK GDPLESTCRHATVTGQGLLEFA GGPLQTLFA
26418	56786	A	26565	329	615	TKTEIGTRSINELRQQLFATTNT FFFPSIFGESNTTSTSLTLKNSAI WCPTGTKLPEGRTGSNLCCSAA SAGDTQANRVWSGPSAN/C*QT CRRRSC

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26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTA AEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSAGFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGK DFVRESPGGDRLNVGQTHKHR GLGRFAQPHGTSAGTSHCGSSS GAFSSWPCWTA AEPAARKRGR PAGSWSSPATGAPGRCRHRILS RGAGGSAGFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVIRSR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCCCRRPLWAGPT SCAGGCGCCWGP GPPAELGPD TPAAEEAAEACCWDAAIFLA
26412	56780	A	26559	448	576	
26413	56781	A	26560	513	782	EIWWWAWTKWGCWVVSFCF HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWISLR SFLCNESESCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNPR HLLHLLPSPLNVVDRLCSCQHH HHQ*CHHLHHNLH*NHSHHRH HHHQ*RLPLHYHLHQHHHHHQ NHCQQHHHRYHQHHYQHHDH HYRHHPWLAGARALCDSND AGCPGSTGDGWRPYSADSDSL DALSFPRLPFPDCQSLRGLASA VIQGYNWLVLTENHILFHLF

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26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPRRTSWG SLVKQVNESNGSRLLRTSLVHE DLEGVSVVSGMNCDSALARYII ILETLIIYLISPRCWIIDSSGACSG LAMYLP LLGDDGVLLCTPNFM AWRSNRTQFMMRSSHMVVDAS PRGRHMSPREEAFGYSSRASHM LLSLLAPPWPQLMGRGLGCQQ QERPQECVPLGMTRSPYSEIHF GSSRALGSSPGSCAHEVLGPSIL TVNPFIPGSSVHVWPSNGNETN KLPHTRAGSCGSATCSVKRWG PQKPRPLPKPPLVPQALLLVRG PAAAREEAVQPPKEEVTQRPGG HSSPGVFAHLKGPRSVVEIRME YGEE*PPGRCVTSSFGGWTASS LAAAGPLTSRRAWGTSGGFGR GRGFWGPQRLTEQVAEPQDPA LVCGSLLVSLPLLGQTCTEDPGI KGFTVRMLGPKTSPAQDPGED PRAREEPKWISL
26406	56774	A	26553	1	382	FRTSCRQLSAAPPPARSPLRPPG GG/EPAPGRTSRGHRPQM*SGT PAPRPPARSTVSPASPLPKPRAG RCGSRPRSACSTFRPC*SLASVS SAKTQGWKMWQPATERLQHF QTMLKSKLNVLTLLKKEPLPAVI FHEPEAIELCTTTPLMKTRTHSG CKV
26407	56775	A	26554	797	1213	AWLKFLLGTRRFLRFSKYSFSID SARSLVPGRWPAPGRTSRGHRP QM*SGTPAPRPPARSTVSPASPL PKPRAGRCGSRPRSACR*GAPG SRGPAFPRRTPSVTRWALGLPW LQGLRTAFCWQILSRVTAATLP DKIH
26408	56776	A	26555	1002	1655	KEFCIYNRNPACSYGVAVG LAFLTCLLYLALDVYFPQISSVK DRKKAVLSDIGVSGEPHPAGTP CTESTEGCPGHRRRKDNPLNEG TDAARAAIAFSFFSIFTWVSTAT AHQPTLVFP*APGWVFPAS AQP*ASPACRGRQPCITPGSEVA GAPSTLGGQGRHYMDPSQDSS MPYAPYVEPTGPDAGMGGT YQQPANTFDTEPQGYQSQGY

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26400	56768	A	26547	3	1215	QTMYFLTPILVAILCILVWVWIFK NADRSMEKKKKGEPRTRAEARP WVDEDLKDSSDLHQAGAGGN AVEGVDQSKVNGRATGFASKL DIGKRRREGELETGSYPKTHA YALKKSGPWNPGTWQHRKIVR GLQFYTVFFPHSSVLAFLAPVID PSVASSSSLRSTTDNELAELSE FADADEWQESEENVEHIPFSHN HYPEKEMVKRSQEFYELLNKR RSVRFISNEQVPMVIDNVIRVT GTAPSGAHTEPWTFVVKDPD VKHKIRKIIEEEEINYMKRMG HRWVTDLKLHRTNWIKEYLDT APILILIFKQVHGFAANGKKKV HYYNEISVSIACGILLAVF*NAG LVTVTITPLNCGPRLRVLLGRP AHEKLLMLLPVGYPskeATVP DLKRKPLDQIMV
26401	56769	A	26548	3	263	RPGEMACKYPLRCSGARVERL AKKKAHACLLWTATIKVITNSV KLRRSS*GNRLKPSILC*DMKA LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS LLWTATIKVITNSVKLRRSS*GN RLKPSILC*DMKALRQYPMPLR AWLLPMVVRVMV
26403	56771	A	26550	91	714	SESLVLVWCGRVSCVLFVCVD VCVLVGGSGVAVRCFGGRGCG PRRVGRRWSCWGCWCGAVLIR RVCLAVMFGLALCVHPLLYPR TLLLRGQKVDRFTNLSSGESL VTLVIFPAHGLARSFNLNDVL FGVHFIAVEFWHAVGLIVNKQ VKGKILAKRINALIEHIKHSKSQ DSFLHCANEQRQT*QCAGPCM GPEPRQACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSRP FRKHGVVPLATYMRIYKKGDI VDIKGMGTVQKGMPhKCYHG KTGRVYNVTQHAVGIVVNKQV KGKILAKRINVRIEHI\KHSKSR DSFLKR

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26395	56763	A	26542	194	558	GCDRPSRPRPGAPRPPAATASC PPRSCWPLVSPHCP*PCRKRRY PGERRTSPAPPVPPGPRPAG*T PPCELRPSSSTHVALLGLALPGSE GTGLRTSVRARDRLHRRTRERA AAGTAPGP
26396	56764	A	26543	1	248	MVAIHNADDAKACWGDVEQLE LSFTAALPVLPHPSLPGERPLQE AVAFLCWLLVDVLLKATVSKV GGGSALASVARVMKAQAFSPL LRILHKASTSSFRARKD\$AHTPS CLLTPSGPERAGPLTQDSCQPSP HDSFRAPALLEPSSALSTAVASL RRREERLEPEQRVGELGSLGER QHEPSDNHDFQPKSKQEQLQK TLQPSGGPHCSSLLLMVFWWK QWRKTEPLKAERTGYKEKEIST KCSSSPSGQLSQSSAAGPAWPE DARPEATWSATLLSFDPRCKND SIEEPCSVHISCTAYS DPLKI HNS YRECGLCPEVNLEVADPSSSSR ELWFRAGA QGAGAMQGVTEL RPPEFVKSRKPQVGSGHMGNC LSKGKRFLGHCQYKQGLPQRH QLQAEERESGMRHTTGGAYAV LTTGVSPWWIWIWERRWPCAF PGKNEEPAGKVPFPSELVLTQ RC**CQMLGGCGAIGALIHCCS ACAASPFSPWRKAPPRGCCFSL LASGRCAPEGNCLKGRRQRT CQCGSGYESTGF
26397	56765	A	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW APVRPEPPR*SPPAPQRPVPSTT QGLNCAGAGHGTGRQLHR
26398	56766	A	26545	1162	2027	MTPEPEWSLS*VGNYKRTVKRI DDGHRLLCSDLMNCLHERARGV SRADPTMAGAE*PAASLPCTGP QYGTVEKAWMAFMSEAERVS ELHLEV KASLMNDDFEKIKNW QKEAFHKQMMGGFKETKEAE DGFRKAQKPWAKKLKE
26399	56767	A	26546	1	504	

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26387	56755	A	26534	1	1758	MHKYVRYSTVHNSEDMESTQ MSINDRLDKENIIHHRGILCSH KKKQDHLVLCCKNIGEAGNHYPQ QRNTGTEKQIQCVLTYKWKLN NKNTWTQSEEQYAVGPVGGRI GRLTNNRHTQDSESWVRGVTA FWSRGANNALDIPAFIIFSEGR GSLHTHDGPPGPTSSLKLSFSHS FDSTGLCRPHDLVLGLIPTMVN ITSQLDWLEDAQMAAGEALFLE GKLTTRKDIYTENPSLHHHHQR PKVDKTTKMGKKQNRKTGNS KTQSASPPPKERSSSPA TEQSW MENDFDELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAMED EMNEMKREGKFRDKRIKRNEQ SLQEIWYDVKRPNLRLIGVPES DVENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKGRVTLKGKPIRLTADLS AETLQARR/DVGANIQHS*RKE FSTQNFISSTQTKLHK*RRNKILY RQANAERFCHHQACPKRAPEG SAKHGKEQPVPA AAKSCQNV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTTPIAGALL PLTKEQRGDF*KPSRNMRTSCW KTPESRANFLKFRPRSHCLTRM GSSCLLPSTCLSSSSTFHH
26389	56757	A	26536	237	415	RCLQRPSAGTAGHPPSAGRPL AAGLAG*RARHRSDDLPGSAASS QESWCLRAALPEAPA
26390	56758	A	26537	373	691	
26391	56759	A	26538	2	233	
26392	56760	A	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	A	26540	184	434	GGRRGCTVGEAAVTQSLSLCS HEGRAIRHQSDASIVLLDQ*Y TRHPVLDKLLAWI*ALAEDKAT LGSIAIAEWKITPAFSFP
26394	56762	A	26541	466	683	GRPHSLPHPHADSSELTTDCS* WRWIFKHKTDIRHQRVHTGQ KPFKC*Q*GKAFRHSFDVTKHQ RTDAVGLHQTCCLLGGVLLWGA HWRGHPYSYSLWSAHCCQHGG GASGGGLSLHLDRSLDAAGRP QPVLPTGQNILVGPLPQISLCS RSLCVLRDLGSLQSPGEEGSH SQKWTSQEVKLFRRSRHQSTSDV



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26380	56748	A	26527	2	397	SCCSDWSAMA*SQLTAISASWV QAMLLPRRPE*LGGSNPEGTG* SERRLCHYA/HSLGDRARIHLH KKGRQEGSKEMSRAQTRRVW HATMETEQKQNYGRL*CCSPST NTRRRTSMRKNKAIAREIERYS KGI
26381	56749	A	26528	312	1061	QQTLYSFGVSFYFSSYCLIFSHG CSSSSICRRARLYHWAAPFRPP GRKRRDCTGQRKTSAGEPEIPP PLHHHHHHYSHHHHRHRHHH HHHHGLQRSSKNFLLWPE*ILF CGSRRLGRAALFLLRSFHPAK QGAESLLGKQS*KHLASTQCGP RGRGS*EKWPRAQLGRKQPSES AAGAAGLAHGPDLSVLERAG EK*SGLRGEGNRPFGGSSSLGG HPLLQRSPAESSPAGTGVRTSH LEGRPASFR
26382	56750	A	26529	161	453	SSSLPCSPSSCPHTSFFLDARQEP RTCRVVGKEL*KKQGLPHCR* QEREKSCSPSGPDLGAPQRA VTPSLGLCSSWHLQASRRHCTP RCPQWKR
26383	56751	A	26530	301	630	RWKPKIRGSEGSAS*PQGR*LLP SGRRGATGSAESTLPKAESSAG DGPVPYSQGSSSLIMPRPNSVA ATSSTKLEDLSYLDGQRNAPLR TSIRLPWHNTAGGRAQEVKA
26384	56752	A	26531	1	1394	
26385	56753	A	26532	240	1150	LLLHVPSPPASTGPPSCGPCWP PRSAPAAGRGSGLAGEDPA TTHKSAGTGECHRGVGHCGQ AHTGPSYPSGPPASCGPAASAV TRGQSCRSLTFRPGRHQIPGAE* QLPRGQGETGRTGLGHYLTLLS CSSRWPLPKSGDGSPSRWEYRD S*ERPGRRTAPRCCSRSTGLGD GLKKFPSSY*GP*KCAPSGCGG QAPWSAGGSTCPPDART*MPR ARARSWAHTGRPCFPRLSIQA TP*RTGGRTCGFCLAS**GSRRG RPSSAESLPAPPGCGQH**PER SARLSWGGGMRGPR
26386	56754	A	26533	1463	1627	

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26368	56736	A	26515	230	561	VRTRHLFCEAAAEEPTPVFTMA NEKPTEEVK TENNNHINLKVAG QDGSVVQFKIKRQTPLSKLMK AYCEPRGLSVKQIRFRFGGQPIS GTQRNLS*KKESVDAASFIVVL
26369	56737	A	26516	1242	1415	NSPSDSSLVWAWRRPQSRWS ERGGGANNRGGGRLLGNSVFG RK*LPHRRVSRVPNTK
26370	56738	B	26517	1	585	
26371	56739	B	26518	258	1081	
26372	56740	A	26519	42	275	TFAWSEEGTSPPSIQSSWDPRCP HRNTPAQTGKPPKRAWPRHPV HH*EPHGDQQDDGPAVSP*SY SQYPWPEGLDV
26373	56741	A	26520	646	1905	
26374	56742	A	26521	6510	7361	
26375	56743	A	26522	1	879	DCQDKVPRRKEPSMCSGLLRV KSWVSLQTYWKPRATQGVVY LPLTEERMVVLGASRVGKSSIV SRFLNGRFEDQYTP TIEDFHRK VYNIRGDMYQLDILDTSGNHPF PAMRRLSILTGEAHWCLGWGG RARAWVRSVLGT*QILEVKSC KNKTKEAAELPMVICGNKNDH GELCRQVPTTEAELLVSGDENC AYFEVSAKKNTNVDEM FYVLF SMAKLPHMSPALHRKISVQY GDAFHPRPFCMRRVKEMDAYG MVSPFARRPSVNSDLKYIKAV LREGQARERDKCTIQ
26376	56744	A	26523	2	478	
26377	56745	A	26524	120	1167	GHVGHMCTGQHMASAYVGRV NVL RKEVD RACFGEKAKQ*VG S*EELWAIWGQGREVCLGIEEA GAHSTRHCNSQNGVRVWAPYL WALEAAPV*VQDRSSPGSQACS LPSPCALTMTGTGIMPLYQEAK WKPRQRPGTSGGTVSSEPHC*D AGSGCWLCQPLREVAHVSAE ITYTSKHSVEVQVNVMSENILT GTSGSDSVDWSSKGRGYTAAS LLRAEDAPGPGPKVLEVPV RCPFYFSLGGRWQSRGHLT*LE TKWRNGDIVQPVLPNGKSRGH QQQVPLLTGDA*EAGALHGFV HGGKKEAPWPLHSCPLAHCCFS GRYNRPGAVAHACNPSTLGDG
26378	56746	A	26525	225	438	
26379	56747	A	26526	216	364	

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26365	56733	A	26512	161	2150	YLD A E K M G Q K A S Q Q L A L K D S K E V P V V C E V V S E A I V H A A Q K L K E Y L G F E Y P P S K L C P A A N T L N E I F L I H F I T F C Q E K G V D E W L T T T K M T K H Q A F L F G A D W I W T F W G S N K Q I K L Q L A V Q T L Q M S S P P V E S K P C D L S N P E S R V E E S S W K K S R F D K L E E F C N L I G E D C L G L F I I F G M P G K P K D I R G V V L D S V K S Q M V R S H L P G G K A V A Q F V L E T E D C V F I K E L L R N C L S K K D G L R E G G A S P G S L R L A A P G P P L T L N A A C P L R L A V L A A M A A A A L P A W L S L Q S R A R T L R A F S T A V Y S A T P V P T P S L R V D D L H L T E I V G M L D S V L T P E D S S G K Y R F I S G E V L C R I T G C F T G V R V E A K D L F G G C C S N P N E V M V T W I K V I V E K E V W L Y L R Y I L K A L P P R T E K M A V D Q D W P S V Y P V A A P F K P S A V P L P V R M G Y P V K K G V P M A K E G N L E L L K I P N F L H L T P V A I K K H C E A L K D F C T E W P A A L D S D E K C E K H F P I E I D S T D Y V S S G P S V R N P R A R V V V L R V K L S S L N L D D H A K K K L I K L V G E R Y C K T T D V L T I K T D R C P L R R Q N Y D Y A V Y L L T V L Y H E S W E Y W K E W G K K * D * S R H G K S I Y G E N S S S E R K Y P G K R F S R * K L L R K N M G N * L K K S S L G T K E I E E Y K K S V V S L K N E E E N E N S I S Q Y K E S
26366	56734	A	26513	3	1186	P A S T M S I R V T Q K S Y K V S T S G P W F F S S C S Y L S G P S A H I S S L S F S R A G S S S F Q G G L G R G Y G G A S G M E V I T A V M V N Q S L L S P F I D K V Q F L E Q Q N K M L E N K W S L L Q Q Q K M A Q S N L D N M F E S Y I N N L R W Q L E T L G R K K L K L E A E L G N M Q G L V E D F K N K Y E D E I N K Y T E M E N E F V L I K K D V D E A Y M N K V E L E Y R L E G P T D E I N F L R K L Y E Q E I R E L Q S Q I L D M S V V L S M D N S H S L D M D S I I A E V K V Q Y E E I A N R S W A E A E R M Y Q N * Y A K L S Q L E A A L Q R A K Q D M A L Q L H E Y Q E L M N F K L A Q D I V I T T Y R K L L E S E G S W L E S G M Q S M S I H M K T T S G Y A G S L S S A Y G G L T S P S L S Y S L G S S F G S G A G S S S F S H T S S T R A A V V K K I E A Q N G K L V S K S S D V
26367	56735	B	26514	361	1215	

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26361	56729	A	26508	31	202	ILITYIHKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQFL
26362	56730	A	26509	471	1716	FKRGQYGQLLRPRFHHGQILYA RRQGADAAGDSDFCTEWPAAL DSDEKCEKHFPIDSTDYVHH GPSVRNPRARVVLRWLRITLH ESAAVEGLAVFPARRHREPEY SIPSPQAFTPAVLATRVTGQLG GHTQIQNPVAPTILGNTPTFHL TCFRIFSLPRHLFPKDKWRTL APFLRTLVLGTESSVHLSGIDP DLLVFEQSPTYLNTRSSSNRWD RLRILKAMNLDKQTTINGMLP STEAPSSSTTHQDLVVNTNSTSY SKELTTDFWARFTSLNESITTKI NKVSPSTDFISNPDNKTISPFEP IDTKLSHMPVPPGLNSSKQLLN KTKGYNSRNHTSANEDSVSVT SKTWLVSVLCTSVIFLGCCIVI LASGCCGKQQGQYKPGQRKSG SLQIKNRNHMKENSS
26363	56731	A	26510	410	867	LLTLRSTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSSLNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISFRVFAA GQGLLGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADRTTRIERPPKKK GTTSLGQRKWLLTQDWPSVYP VA\HPFKPSAVP\LPVPNGLSSK KRACPWQ*EGN\LELLK\PNFS GF*LPVGN*KSTCEALKDF/CAL SGPAALGQWTRKC*GR/PFSI*I* QH*LWFHQDHPVRNPRARVSS LKSKAFSV*I*HDHAKKTLITLV GERYCKTPDVLTIKQNRWPLRS QITIMPVYL

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26353	56721	A	26500	1	465	VSPKLLPSYASRPYLVPNALSSP SVPPALSASSAPPRPATRRRPPP RGLSASWPLRRRSRQDAGAGS RRLRERQNRGRRRSDLAPTLGA GLRRDRPGRQPRPGKALAPFAV PRPRTNFRGRS*KSGSQRTTRTP RREICRTHSRDRPRKLVGRGT ANGARALPGRGWRPGRSRRSP APSVGARSERRRPRFWRLRRR EPAPASCRLRLLSGHEADRPRG GGLRRVAGRGGAAEAESAGGT LGDERALGTR
26354	56722	A	26501	1	1344	
26355	56723	A	26502	548	689	LGKFAPGLTASKAEATAAELCL KYPLEICTFL*GCVVCVCVCVCV CVL
26356	56724	A	26503	154	476	TLA*AAASTSCSPRPPPPSPAS TTTRWRAPWRTR*EPPESLCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL
26357	56725	A	26504	920	1420	TLA*AAASTSCSPRPPPPSPAS TTTRWRAPWRTR*EPPESLCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVL CMTVDL*LI PTSTPTT*PSELLAPSPNSPIDTT QMSGLTATSVPKKLAFSWQQL CYISLIQPLSL
26358	56726	A	26505	1118	1403	AGWDPSFLISFGLSNAISSSSSS LSSQ*ESNASE*YSSATSGSSGIS WYPRSDVASSTIDSSSWRSMEG IG*DSGRFSKVGSSDSSSLPCHL SS
26359	56727	C	26506	29	379	
26360	56728	A	26507	3	948	GVSLCCPGWSAVVGSWLTAAS TFRAQAILSSSWAYREPPVRVG RRQPPLLLTRAQGRVISSSRFH LHDFVWRTAGKESTSGANETG PLPERGRRPGGRGPGSRSPRSH AVQREGAAGSVPAAGR DGGRA GHDVPHEGQRAEAAAGEAGGE FPLLLSDRRGRARRSPAAGALQ SRPGRARHLLHQLH*GP*EEVS L*VQQRGAVSGVDGGSASGQL RVHA EKAHLLQERNPEG*RAK DPLGTVSALSEEARFQLRWLAG VSAGHGGQRAAGRDWPCPAM NRLAMPGSVLFWFLVFGSGFH CVAQARVQWCHSSL

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26347	56715	A	26494	375	1327	QPYFPMETVMTLEGGQKPVME SYTLHYLPCLLCPLWRNPESSE WQRQLLDFPLASAPGSLTQH MAAPKSGQNLEAKPKGQASLV LSSRKICGVLSGACAACPGGPA R*VDPAIPFPLAGEAGLEGRPRP QRCAAKWQSRDLIPGLPGSTGL PFPPY/PPCSPGALLSQSPQAAG SLLARTPHAQGCPPRLRPARIL PWPASSARRYTPQPSRKGTQRT PFFSLNLLTTTTASYSLDFLLTA PEGFSPLFTASQEHDQNNQEH FLLQDEGLRSPVKTRARLPLGL HGDKVEKAGPWSLGARESNC SATSQRSVAAGVPRAQPLPPK GKGWLDPTWQRRDRTQRTL SIHHRFYGYSGWPGPLALLQ GFVRSLELPCAGSDQNRGQRLK GNPGAFAIPKTLDFSKAGKED KGGNGVCTTPSQAFDPLPRSSQ SPLGNMAVSGSSSGSWKSSGT QEKSLNQKRKVDEAEKKEEK EKKKEPEPNFQLLDNPARVMP AQLKVLTPETCRYQPFKPLSI GGIILKDTSEDIEELVEPVAHH GPKIEEEEQEPEPEPEFYIDD
26348	56716	B	26495	1919	2074	
26349	56717	A	26496	179	431	PPTSLIRVSTSTSTSLCTSWLCS SLSWLYSWAGPFFSGKMTASC RSGSQINREIVLMLLLRS*VFVV ISPLEGGSETSPFMDL
26350	56718	A	26497	37	199	DGLPGLALGLDAQASWSASVV TGHRPPAPPGLALGGCHGPAAP P*SGPAGSPCH
26351	56719	A	26498	3	224	TGHRPPAPPGLALGGCHGPAAP P*SGPAGSPCH*TAPRGAGTPLP GSRRTGTSPWPHPPGLPHIPDVT GGHRH
26352	56720	A	26499	151	403	MPRHRRSASVVTGHRPPAPPGL ALGGCHGPAAPP*SGPAGSPCH *TAPRGAGTPLGSRRTGTSPW PHPPGLPHIPDVTGGHRH

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26343	56711	A	26490	105	849	RRQDSGQSPA WPAGALLTLLT HCAVPGSWAQSVLTQAPSASG TPGQRV TISCSGSSSNIGNNPVN WYQQLPGTAPKLLIYRNNQRPS GVPDRFSGSKSGTSASLAISGLQ SEDEAQYYCAA WDDSLNGSYV FGTGTKVTVLGQPKANPTVTLF PPSSEELQANKATLVCLISDFYP GAVTVAWKADGSPVKAGVET NKPSKQSNKYAASSYLSLTPE QWKSHRSYSCQVTHEGSTVEK TVAPTECS
26344	56712	A	26491	129	1191	RSRPQCLGPQGRRTISCTGSSS DIGAGYDVHWYQQLPGTAPKL LIFRNSNRPSGVPDRFSGSKSGT SASLGHHWGS RVEDEADYYLP VPIDSSLSGSTVLQARGELRQEP TSSSARRSMKKGRDLGEAQLQ LRVEKTGLRTISSMAWSPLFLT LITHCAGSWAQSVLTQPPSVSE APRQRTISCSGSSSNIGNNAVN WYQQLPGKAPKLLIYYDDLPS GVSDRFSGSKSGTSASLAISGLQ SEDEADYYCAA WDDSLNGYVF GAGTKVTVLGQPKAAPSATLF WPSFEDASDDEAEL*CAIRDYY PKAVMVA*KTNITPLKQGKDT SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	A	26492	283	840	TLPAGFTDVISIHKGTGENFC LIC GINGRFAVHCITLEEAKYKLCK VRKIWFHDAHTIHYLDSFVKVN DTV*TGKITDFIKFDTGNLGRIG VITNRKKHRGSFDVVHVKDAN GNRFAPWLSNIFVTGKCNKPWI SLPRGKGIRLTIAFHSDKWFCSD ISVQNLCKRFSQGDGTGIKNSEA RRCSNLQV
26346	56714	A	26493	1	843	MARGPKKHLKRVAAPKHWML DKLTGVFA PRPSTGPHKWRECL PFIF\LRNRLKYALTGDEVKKIC MQRFIKIDGQVR\TDITYPAGFM DVISIDKTGENFR LI*LTPKGS AF A\VHRTPEEGQVQSCAK**RYI VGTKRNPFI*VTHDAR\TIR\YPR NPLIQGEMDTPFQIEFKKTWPR LT*FPSKV PNTG*PCVMVTWRC LTLGRI\GVITNRERHPG SFNV VHVKD\ANVNRFATRLSNIFVI GKGN\KPWISLPRGKGIRLTIAE ERDKRLAAKQSSG

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26330	56698	A	26477	131	544	TGRPLPRPLKTQEIPSGCGVMG RATPGTSGLGDSVRRVRGAIPA PRSSLGRGFTCV*LTTGAQLAPS LVPAAPRLPAALMDIQPEPLAS AAPAATGPAQVTAATPLTTASA TPLTTETACSLGSSAASPLAPRA HCV
26331	56699	A	26478	1440	1877	PFQNLQFQNRNERTSCLCCLCMGA TWASLRALCCSPSP*HGWISW WWSTPTPFANGSVTSCSALTRS RWRPTWSEASGLWHAPAALL WKLRPLTPCFRSPISLSDLDLTS HHQQGAPTMTCLGVGSSSWE LQAIFVLSYWFSPLHC
26332	56700	A	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI NFPMK*EMIPY*KLS*IQNLFQF PKVRPKGSQFGQVKH
26333	56701	A	26480	392	634	
26334	56702	A	26481	416	601	FLITDPRIWKASSDPSAKLFTFP SGFLM*AGTWMKLETIVLSKLT QEQTCKHCFSLISGS
26335	56703	C	26482	34	279	
26336	56704	A	26483	173	307	
26337	56705	A	26484	196	527	SAVAAACSRPEEDAMELVLF LCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFS VGILLILSRCKCSFNQKPSGPR R*GSPGGRTSSPPMQQKPQKAE
26338	56706	A	26485	597	797	PSENELKALGYTSSAWKRFSEQ QWGLSLGSSAPSWRLPW*GDW ELPGEPGGDSSHRPFGPIPRAP
26339	56707	A	26486	3	184	
26340	56708	A	26487	256	635	GCVAPQIREQHAQSTENAAKPT RRIHSRQSEKPGRWRHGWRA GWRRSKRAPARHRPCPAVCP RDGEDCSREAAGA*GLSGSSAC PTSSTGASCCFCVPGQLNSVGF AVLGSKVLWTPGESPFQ
26341	56709	A	26488	1	378	
26342	56710	A	26489	1	571	



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26327	56695	A	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV EVDLFTSEGLFRAAVPSGASTGI YEVLELQDNDKTRYMGKGVSK PVEPINKTIAPVLVSKKLNVT EQ EKIDKLMIEMDGTENKSKFGAN AILGVSLAACKASAVEKGVPLY HHIADLSGNSKVILPVPVFNVIN GSSHAVTKLAMQEFMVLPVGA ANFREAMPIGA EVYHSLKNVIK EKYGKDATGVGDGGAFAPNIL ENKEGLELLKTAIGKAGYTDK VIVSMDVEASEFFRSGKYDLEF KFLDDPTRYISPDCLADLYK SFI KNYPVVSTEDPFDQDDWGAW QKFTASAGIQVVEDDLRVTNPK RTASAVNEKKCNCLLLKVNQIR SVTESLQACKLAQANGWCVM VPHHSGETENTFITDLVVGL*PG QLKTGAPC*SERLAKYNQLLRJ EEELGSKAKFAGRNFRNPPAK
26328	56696	A	26475	2	684	HSGSSLLHFPILLINRKGFSP TG MISLMCNRIVLSTHAKLQ SCTP SNLPSQLPIGLSMSTPTKYRKLS FPGKTSQNITVPDSIVSPTFKETL EFISKGGSSSTCIVSPGPA*SLSNA VSSSSMSSSLSNATNTPQSSSH* KSCFPWYTPSVKP*PRPSSSNST PKNIPETVLSANRGPLKRTTPG NFSSPDLSCFTTGQPPSIWRPLL KLVSGFKQAEPLLTIGNCQK
26329	56697	A	26476	1284	2339	APPSARGACAASRRAAVPALPT PPSVCSGSHMSTYWPAAPR**T PGSSTAASPSAASRAPRAASPV LTASPPLPAASPSAASHAPPAA SPVLTASPPLPAASPSAASPAP PAASPVLTASPPLPAASPALAAS PVHTASPPVHVASPPVHTASPP VHVASPPVHTASPHVHVASPPV HTASPHVHVASPPVHTASPPVH VASPPVHVASPPVHIASPPVHT ASPHVHVASPPVHTASPPVHVA SPPVHTASPHVHVASPPVHTAS PPVHTASPPVHVASPPVHVAYP PVHVASPPVHVASPPVHVASPP VSCSGDSTSDCFPPQPGAVFPHS LAPSLGGWSHLVAALP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26318	56686	B	26465	18	123	
26319	56687	A	26466	19	347	
26320	56688	A	26467	3	746	SRKLLSKSVP*LNP*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGLRDISWLGTDDR SASPQRLAAAAALTAGNGRRCSS GPRRRPPP*PLARPRQRQPPER QPVVWPPAFPARWAEHTCPLA PWQPRSPTTPSQPAAVTARAS
26322	56690	A	26469	1	420	
26323	56691	A	26470	65	330	RDCEARCARGPFWWSLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	A	26471	327	981	ASYQKFFQLLPDCNLAPSPHPQ VPATPSTSWGHLSKPPGAFRKR HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQLCPQLRVS PLTTGSLPPRSREPPRTAPPSPY PNCRPLPKSTRTPSVGWSGPPSC GTRLQSHPQEAPAG*GSVRRPF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSPSQGAGATMGNVG
26325	56693	A	26472	336	923	LKNIFLSLPR SINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHAVCLKCL *KPSLLSLL*DI EYIRSHYNIEDFI YFSHHQREEHGHMHFALNPIF RHYTKFFLKVYL*SCTQTSVLS LSDILSPKI*IAVFQFQNPYAHSL TSALHYLVPVRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	A	26473	97	298	DNLTLLPRLECGGMIMAHCSLN LTFSSDPAASAS*VAGTTGT*H HAWIFVFLCNWLRNRGVTVKK RS

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26311	56679	A	26458	609	1031	VCKSYPGHQGSSCLPDGQIQWL LHGYGQEFCEGQETHPFLDG*RG AESL*GHNSGHDQWCLGDGCC WGWLLTYERHEQLPAELEAPG GWGKDGDSTRGTESTC*EAGAG AGPAHPAPPAPAAEGEPDLFQL PGQGCSRIPCG
26312	56680	A	26459	1	393	
26313	56681	A	26460	357	843	QTEGGAQTDGQQSQTQSSENSE SKSTPEDNKICG*KPDHK*TFLF YQEISISI*RCACFPFSSRCMQGF GFVTFEKCENFMFPNVVHFFPAL FSPCYDMH*SSLSSNSLKCLPSI VVTVHLLLNAS*NFCCHILGLPL VPGFPYPTAATTA AAFRGAHLR VFV
26314	56682	A	26461	3	1172	GRAHGEAAADCGGGMQNEPL TPGYHGFPAARDSQGNQEPTTTP DAMVQPFTTIPFPPPP*NGIPTEY GVPHTQDYAGQTGEHNLTLY GSTQAHGEQSSNSPSTQNGSLT QTEGGAQTDGQQSQTQSSENS ESKSYPRNGLHVSYYFLSGFRD P\DFRQMFG\QFGKILDVGIIFN* RGSKVNNATARVMTNKKMVT PYANGWKLSPVVGA VYGPELY AASSIFQADVSLGNDAAVPLSG RGGINTYIPLIPGFPYPTAATTA AAFRGAHLRGRGRTVYGAVRA VPPTAIPAYPGV/DLPGTDFTVL TSMVDMQPTDMHSLLLQPQPP LLQPLQPLTVTVMAGCTQPTPT MPLPLPLAMELALWRVYTEVA TADLPPEVTVKPLQMGQPPSS
26315	56683	A	26462	1196	1459	KQCQRRCLETEVWKL SKLQIST KASNRQDRSTFSAPPRKSQLM W*TSLLSYFQKLQSPQPSATT ALISQQPSTLNPQPWPGSCPGG
26316	56684	A	26463	2234	2702	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQKGGVSGDGRSSCR RAVAPLEVPRAPEAA\ARPRPP SHGRDPPPGDPPLRTPASAM DKSAGTSCRLSPLKALGSARAE QTMGRPAAERSYPLLRAYSSR
26317	56685	A	26464	70	398	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQKGGVSGDGRSSCR RAVAPLEVPRAPEAA\ARPRPP SHGRDPPPGDPPLRTPAS

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26302	56670	A	26449	1041	1410	QEERGKVEE*ELEGRRREEKRR GRGRRGSGLEEGRRRRRGGG DETKDKR*RKRGGRKEKKEE RRRRRRGGGAACKEEEEEDRLP TRAFSCVEQQSASKSPLVELHP GPIPQGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPQA*K RPAEGAPNPRGPRRKEGRSGAK GSLDTGDGGEAWWAGSPHPS WP
26304	56672	A	26451	111	540	LPLALSNPKQEVVSGRGGQVDS QAGLTMGTGRAVCCLQLCLNAS GAGDAEAMSAGPPGPGPARAD TEQLPSPSLPQVS*HWRGSASTS ATRTWPLRRRCSSMARSTCRAS ASASAGPWPWPGAPVPWRHSA EPSCSQLPGPSA
26305	56673	B	26452	57	558	
26306	56674	A	26453	804	1524	ARETSHGDFLHFPLIWLFLSLKG NVPAARINIMNWNQGLISHVGE GNVNRKHDVIGFNFPWNCLFN VSDLVTMIGSPQRNHFGLVM VLTGIHTFHRHVGHCRCPWS NQASHQKGGDDLEHEQNPTNNA QLLGAHVFYNCPRPFLRPPFFFS P*NKCFRGELFAPSSHHSPSFLA SFLGAAKLQRCWSAARMGPGR KAPARIPPAQPARVPPMPGAVI VAAPPPVDAPIVRICVHVCCLHH
26307	56675	A	26454	2	330	SCSRSGTALGVPVLAGPVRSA TYLPAHSAGQRHQHDAGPTRG LGAI*DLPPVVTPEQSPSCRQ DQVPIVAAGE/PRCAPSLGSPG LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	B	26455	1	969	
26309	56677	A	26456	43	568	RSRLVFPLYFHASQGPGTASRE VPGGWA WGPVAQRINGICLLH STGPEAPSTMPPPTRLCGGPCG ALPFSSQLAARGNPRSLPAAQL RALLSKISPPVVTPEQSPSCRQ QDQGADCGKQVNKMCSQAWG SPPGLELCPCCHQ*AGPPRPPSCP LSG*FVLRTGAPGAAPPSGTV
26310	56678	A	26457	1	456	HEDAASSFQADVSLGNDAAVP LSGRGGINTYIPLIIPGFYPTAA TTAAAFRGAHLRGRGRTVYGA VRAVPPTAIPAYPGVDMQPTD MHSLLLQPQPPLLQPLQPLTVT VMAGCTQPTPTMPLPLPLAME LALWRVYTEVATADLPPTVT

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26290	56658	A	26437	2	787	SQWLKLPSPHAGISRYNWD QAP*KTGGPRESYPYHKKREVM KLGRPSCP/NPKIGPPAGIQHSP VCRGGYQEIPVPLRLDRGEFLP GGSECCTS*NKGSSIVVLQCHL NNGAGFVPKTPGWKEFCIVASS DQQQPYRPVVTSSHLACPLGP QRKGAQAGLLEERRDF*TKKRS VKLRKEI*LKRKNCQNSAVL PGREQFPARGKLS CRA/SRFQGP GQLWAEQDGFCA*EGQKSLEF LSLGKSKARKGQIKSFLSSPM
26291	56659	A	26438	62	872	ANWTEPDDTKTMWRLSVPLDR SPQTQNCTGEPLMPTGRQELPQ RGPEPMEAPAPARPQSRVPAA GPVARQPHMRPPHSKQGEKQK MPGSRWPGQRGRGRWGSPLES A**TRKIFTGIPILPLLPGTPGRP APEEGMQSADKNRVKRRGGTQ RNSALALEFCELLFVSSKWFCALP STLRLKALSAAVALLAGDPE FGVRNVVWVWAGGVRCRVA HRTTEAGAFFPDWFVWVFAAT KRGDGETSGCEHSEPVSGSSGG SPPRGQYLPGM
26292	56660	B	26439	1	606	
26293	56661	B	26440	48	381	
26294	56662	A	26441	16	209	
26295	56663	B	26442	466	1275	
26296	56664	A	26443	2	252	
26297	56665	A	26444	95	266	
26298	56666	A	26445	119	343	CTLRQESKLSRGDLTAPPVSSPR GHRSSKKGGNT*LGSMQL*AES CRAEPPRPALLCPGRSVSACQW GPEGPFF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML LQRPGGVLVGWDPDAAHPVGT *RHSVAQHN*MPW*GAEGMCQ PC*WHGMGTSDGPGLSDSERPE LS/HADSEGRVSKAKQSELGP GQKR*GQKPPKGYRFQERTQR
26300	56668	B	26447	430	540	
26301	56669	A	26448	111	591	PGAPSSHSGPRLLAWEPIVLAP VASLGLGEAEDCSFLGRKAGV GPRHPR/ARRVHSGSRETCRG *QEPRPMLREPVCSAFLRTVKK LSGRVFPPLAVKQVLSAAPAVP ALLRTAPKTPWDGPESAESQPP SLGPAVVLDISDRRKQETIKAT GGPGLRR

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26280	56648	A	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRRAA SHLAPPTPLPTPQTPTTRTRALPS SPGLGRGA*RTVLPSAPPEVPLA WGCRRRA
26281	56649	A	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ *PHPDSGPR*LQ*LQ*PHPDSGP Q*LQ*PHPDSGPQ*LQ*PHPDSG PR*LQ*PHPDSGPR*LQ*PHPDS GPR*LQ*PHPDSGPR*LQ*LQ*P HPDSGPQ*SDSGPRGHR*LQ*L Q*PHPDSGPQ*LQ*PHPDSGPR* LQ*PHPDSGPR*LQ*PHPDSGPQ *LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRLLFS*RYVL VMLFSISLVSFVVISVHVICNYPF ALFFVCASFCCGAGGLVEFVL MIVGDASAALLCMPRCEC
26283	56651	A	26430	524	1995	
26284	56652	A	26431	601	1058	LPSSGGRCRSPKTR*SACLVSGS PRTPAMIRSGAGQPLARSPTPT PPFCRPLTRAPQASSMTWTGTS TTTWTLCAMRTDCTGLPSTSPT WCFCTRSSSWPAATSGSNSRAP ARSWSTLCLSC*SASTRPGPRGP CRRQWWRRATPSRPSAR
26285	56653	A	26432	1	371	
26286	56654	A	26433	71	335	
26287	56655	A	26434	2	416	
26288	56656	A	26435	60	370	
26289	56657	A	26436	466	1454	PCVFQIGPRIHTVRVRGGNKK YRALRLDVGNFSWGSECE*GPL GVGCKTHLNGFKIHRARPALIF LNSAA*EIGAGKDCGLPNITRN VG*GVVEDELMPHGL*RLRVPF ISP*GPHGAEEPGGVCQGHLS LLDAKFL*AGCTRTRIIDVV YNASNNELVRTKTLVKNCIVLI DSTPYRQWYESHYALALGRKK GAKLVRVTS*GLWGGQPDSS LLVMKTLSSATEGREMRAF*A EEGQHWGVQGSRLPGPAFLP* AHIFVSPFQTPEEEIILNKKRSK KIQKKYDERKKNAKISSLLEEQ FQQGKLLGEKADELEVGSRRD

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26269	56637	A	26416	347	725	EAKRRRPLSTLMEKRCFQPLWT RPSRKKPRGRTWRPPALNPTRI AGPPSPPAVSPGFGPIPP*SISCFP KGPFGSMGFLRLRCFSAVQKVL APGSPA*PCLSCGPFRTALGDL ARTPEKLCWLERS
26270	56638	A	26417	525	708	IVAELIQHHQLPCSHPLSGGKIK DQQVVFLSLSP*SSHNTLY*AP KTNQRPQDYPEGNA
26271	56639	C	26418	1	1050	
26272	56640	A	26419	934	1708	PQRGVWVLSVILHFPWLGSGL PNSAGD*AARYSWNQILKPCD* WKLSSAAGISFQRS*VNFHYGE FCPKIPSGMYESKLGSHDTP HFLPAQKTRSTPSPATAPLPAT SPRPPRGRRRRRRCPEQPPPL QAGPTAAARHRQDPLPRFSPLC FHSHPRASGAGSRPAPARVSPW TRRPAAPVSSGRGRLAPKRSLS PRPPRPGQGGGRVPARRELPLA PRGLCVRLVYSLCSSLCGSLPSF SLGSLVFSSSDQG
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCRR*PYSRGT
26274	56642	C	26421	4	90	
26275	56643	A	26422	216	305	ICWKYFCAG*CGKYFTLGPRSH SYRRSDY
26276	56644	A	26423	859	1248	CVISVFRASRKS KHNVI AVVFS YCSVSVGQRPAVP/QHQVLLQT QGISGYPRAGTLTGLHPMQV CRCRR*PYSRGT**/REPS*LREG GSAPPKSVCPVPGACIKRLSSM SSSFSSFPFIKHAHACCRVLS
26277	56645	A	26424	132	548	SSGFSWGFFSGYQRCRESR/CD YPPPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEVWDHGPTR IVGLIISLGPRSHSYRRSDNQTG TTVPLVSSV
26278	56646	A	26425	382	697	YAVKQAKTTFEDMTGRRASLL LHKGYLEFELFLQTAAYQSGSP APQGTWSGTGSVCHCCSLAE*T PFRTTGACCGLMARTGHARAA SICPPDAVAPLSPSPNAWF
26279	56647	A	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI GLHNAGYPGRAGTLTGLHPMQ VCRCRR*PYTILSLQEQTDDVSL N

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26262	56630	A	26409	3777	4343	DQEEPFSGNSSIIQSLFTIKLN PQ SSLQEVCSLDTHNSPVRVFKNS CSAKFHFKFVWNVILLQLSSE ELILSFVIPGVGHCWSSYCYILQ PRIFPLWSFYIVIVYVEDSSICVSS LFPSWR*RP*IIGSIK*CLSSQMG WNFQSW/NLPR/CVVLVLWSIK KGL/HIWCMPDFPAFRKESLLN FRWLGHLLA
26263	56631	A	26410	473	667	PCSDWGWRSWPWNLQLEETWAL *CCSHSHKVSQEGTWMKLETII LSKLLQGQKTKHPMFSLTGGN
26264	56632	A	26411	1416	2108	QRANIQNLRQTQTNLQEKRNPI NKWVKDMNRHFSKEDIYAAN RHMKKCSSSLAIREMQIKTTMR YHLTPVRMVIIRKSGNDRCWR GCGEIGTLLHCWWDCCLVQPL WKTVWRFLRDLQLEIPDPATP LLGIYPKDYKSCCYKDTCTRM FIAALFTIAKTWNPTPKCPS\MI DWIKKMWHIYTMEYYAAIKK DEFMSFVGTWMNLETIILSKLL QRQKTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCSSYYYFKYFFCFFLFSLLLF *IFFLFLSLLFASLLFLASPLCVC YFFFIVVAQFLNSLFHFFSLFVL CFSGLEVSIDISSSVEILSSAMSIT LMGLSKAFLIT
26266	56634	A	26413	181	742	PLLKSGCISFLLRLLVKLYRFL VRRNNSTFNQVVLKRLFMSRT NRPPLSLSWMIQNIKLPDREN KAVAVGTITDDVRVQEVPKLK VCALRMTSQARSGILGAGGKIL TFDQLAPDAPKCGTVLLSGPR KG*EVYRHF GKAPGTPYSHTKP YIRSKGRKFERTGRGLASRGYK NYRSYPLIKDCL
26267	56635	A	26414	368	675	SLSTLLSSRDCPLATISKQLRVL ARGCVVNNCFCKHLLNTCSLA GTVPG*GASSGRQKFKLLAKFK VLARLCSSGSGRGEFSCFLFL GATGILRLMASSS
26268	56636	A	26415	40	355	LLGNPSPVVKGRPCRHDGSEI/A PRVYFRGCS*SSHSWVSHFLSA PSHPRMLPTSRHRPPLRPLT*ER RGKRRDD*PLHHP*P/CWSTCSP STSARATPTPPSGSGW



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26255	56623	A	26402	27	264	RLVEWL*PRDLLNGFDQNADN DMDNEIQAEEVSDGDEELVGN QSKGTWCPVPQLLQLWLKGAK IQFGPWLQRVQAPILASFHKVL SLQ
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRRQELR FGNLHLDFRRCMEMPGFPGRSL LQR*SPHGEPLLGQCRREMWG QSPHTESPLGH*LMEL*HPPSPR MIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSGDQLERKLKKDK ALMGHFQDGLSYSVFKTITDQV LMGVDPRGESEVKAQGFKAAAL VIDVTAKLTAIDNHMPMNRVLGF GTKYLKENFSPWIQQHGGWEK ILGISHEEVD*NIRFVIRNTLCLL WSCARWPSDGPTGDYNVQGR WSIDVFKTIIPVTGEASGEVSFV
26258	56626	A	26405	1	229	LRRLGITHVLNASHSRWRGTPE AYEGLGIRYLGVEAHDSPAFD MSIHFQTAADFIHQNKRAISAL HLCRKSGIRQA*MSIHFQTAAD FIHQNKRAISALHLCRKSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAPRFKTLRRRWVQG QKVLRKAPFGKKPRGSLTFWR ASTRVRDMANNRRELRRLGIT HVLNASHSRWRGTPEAYEGLGI RYLGVEAHDSPAFDMSIHFQTA ADFIHRALSQPGGKILVHCAVG VRSATLVLA*PHAVPPPLPFVE AIKKVKDHRGIIPNRGFLRQLL GLGPQLAAGSGSMRGGGEKLR
26260	56628	A	26407	605	1231	NCSNSGVWRISHKKERSIPDSK RRRSRGNTKSSSPRPTTRSLEKL LTSGSPRIWPVRMS*LHDKARR ASFSSSSSAIKKAFSSASRSSNES VSSLSNSSLEGQSKSMSISSST GVGSRLALGLYTSSEMVKGSSF ILSSSSLGGSSYSRAAFTGELEIK GAEMFSSLGNGTPVLRAVTLEP SLSRRTNTLLQWFPMCNWRL RRVWI
26261	56629	A	26408	771	1121	FSPKLLPRREGKPCAPARTQ TPRSKSSTPPSQV**SVSDPQP KGKQDRSRGGPLQERAQRESG PNLLAATVVP RPRAERHPAISTE GPTGPPEGSAPSATSSVAAAGP APHSR

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26247	56615	A	26394	1	645	MIHEQNENIKKNTKTIKKNQTEI LELKNTVTEWKNLLEVFNNFSFR QNEESVNLQTSYLKSLSRGEKR KKKCEEMIRDLGQYQPGPYMH DGYSRRESGPNVPRRAQVDGG DARKGTHRRKRVLERGLWLKR EDKKAQGYKGR*KGPRV*GTD PQEEDLQRLSAETWLVL*PEPR P*KAPAKKGEKVP*GRKGKAD AGKEGNNPAENGDKTDQAQ KAEGAGDAK
26248	56616	B	26395	1	663	
26249	56617	A	26396	265	735	VMWLRDYDTLSETHMHQLLGL NLLFLLSQD*VAEFHMELEWLP ATDTQTNAYIKRVSLEPYLME GGYNKVFLAKGNIPAKSYTFIHI LLDTIRDEMAGCIEKAYEKILFT KATWILFLNTPKQMMDN TKK* GWVLGPNNYYSFASQQQKLED TTIPS
26250	56618	A	26397	215	386	
26251	56619	A	26398	3	515	QLPESAYMHQLLGLNLLFLLSQ NRVAEFHTELERLPAKDIQTNV YIKHPVSLEQYLMESYNKVFL AKGNIPAESYTFIDILLDTIRDE IAGCIEKAYEKILFTEATRILFFN TPKKMTDYAKKRGWVLGPNN YYSFASQQQKPEDTTIPSTELAK QVIEYARQ\LEMIV
26252	56620	A	26399	423	4482	KLWILFDFICLAFL*FFSTYMY SCE*ILVKLTLYFSFHVYLLIYC ECENLTGTLDLVFI*KCKSLLIW IA*TVYKKIHMEGEVKG
26253	56621	A	26400	173	174	AVSLLKHSNNDLCSS/GFPTSRT ADPTSCGSH\WPWGPQSLKQ*P ELYIGPF*PRLELKQLGCRAPSP
26254	56622	A	26401	135	699	RDLVPCAPAAPAMAKRGQDTV WAMASEGASPNPCQLPQGVPEP AGQCRRKMWG*SPHTEPPLGT A*WESLELPRDLLNGFDQNA NDMDNEIQAEVVS DGEELVG NQSKGTWCPVPQLLQLWLKGA KIQFGPWLQRVQAPILASFHKV LSLQGS AEGKCGVEAPTQSPH WALPSGAVRRGPPSSRPQNGRS TNCLHCEPGKAADTQCQPVKA ARREVVPCAKGAELPKTMGT DLLHQCDLGVRHGVKGDHFGA LRFDCPTGFWTYMGPVAPLVW PIFPIWNSCIYPMPPVPIVSRR

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26238	56606	A	26385	1125	2228	NVMSHLGRPDGVMPDPKYSLE PVAVELKSLLGK*VPGSGAGR CGGGSCQARCYAGSVILLENLR FHVEEEGKGKDASGNKVGVPVIL TLLGVRA*VCKRLWLVNDAF GTAHRAHRYQEPCRLPH*EQYS YLLE*PKYFAKALESPPERFLAI LGGYEELFKIML*VLFAW**AIT WIGGGMAFTFLKVLNNMEVGN KCQVDVK*LSMIIAGCINEKNG VKITLPVDFVTADKFDENAKTG QATVASGIPAGWMVSHLSGLV V*VNRNSVVSFIHFVWNGPVG VFEWEAFARGTKALMDEVVK ATSRGCITIIGKRSYTKLIPI*AG RILIRGRCTGGGASLELLEGEGL LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSA RRQSAPSLTESPTSPSCISKMA LSNKLTLDKLDVKGKRVMR VDFNVPMKNNQITNNQRIKAA VPSIKFCLADNGAKSVVLM\SHL G\RPDGVMPMP*QVTPLEPVA/V VELKSLLGQGMFCS*RDCVSPE VEKACANPPG
26240	56608	A	26387	3	378	
26241	56609	A	26388	311	578	LGIRGQTLGFLSRARCGGSRRS LEMQNNAGEFVDL*VPRKCSA SNRIIGAKDHASIQMNVAEADK VTGRFNGQFKTYAISYFLNLFL HH
26242	56610	A	26389	3	333	DAWDLCRVTSCFLSLSRVWW QQAQPSLEMQNDAGEFVDLYV PRKCSASNRIIGAKDHASIQMN VAEVDKVTGRFNGQFKTYAIC GAI\RRMGESHDSFLRMAKADG IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM QNDAG\EFVDLYVPRKMSAS NRIIGAKDHASIQMNVAEVDK VTGRFNGQFKTYAICGAI\RRM GESDDSLRLAKADGIVSKNFL TGEESQDVGIFCHK
26244	56612	A	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSPRDPQEEDLKLLKFAFSR GPPLSLVHPPPLLSYPSARR*PQ TPPRPPRHPSLHPLHPPSAQP
26246	56614	C	26393	17	319	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26236	56604	A	26383	3	2237	NRRKFSVVSIGFYTVMDAQYKII TKTAHLITKESPOEEGKEMFAT MSKLKEQLTKVRK*FNALLYES QQLLIPLEELEKQMTSFYDSL KINEIITVLEREAQSSALFKQKH QVRTILFKWCNSSQKMTLCLVL GSMISMLSTAKITIAGYKSEVEV SVSHHCI*NCKKTLTIEKGSQS VQKFVTLNVLKHFQDQTRLQR QIADIVAFQVICSPC*DWKKH VETNSRLMKKFESRAELEKVL RIAQEGLEEKGDPEELLRRHTV SPPFRDQRVLNAFLKACDELTD ILPEQEQQGLQEA VRKLHKQW KVSQDRTAYHLLHLKIDVEKN RFLASVEECRTELDTREKLMPQ EGSEKIIKEHRVRLPHHSPHHLC EKRLQLIEELCVKLPVRDPVRD TPGTCHVTLELRAAIDSTYRK LMEDPDKWKDYTSR*PQNGLW ISTNETQLKGIGKAIDTANHGE VKRAVEVSSGSLSKRGETLSWL KSRLKVLTEVSSSENAQKQGDE LAKLSSSFKALVTLSEVQHLL THFGDCVQYKEIVKNSLEELIS GSKEVQEQA EKILDTENLFEAQ QLLLHHQVKMPLSSAKKRDVQ QQIAQAQQGEGGLPDRGHEEL RKLESTLDGLERSRERQERRIQ VGAGS*ERFETNKETVVRYLFQ TGSSHERFLSFSSLESLSSELEQT KVYYGSLESIAVQAENLVKEAS
26237	56605	A	26384	1	390	GTSLFDEEGAKIVKDLMSKA EK NGVKITLPVDFVTADDFDENAK TGQATVASGIPAGWMGLDCG/P ESSKKYAEAVTRAKQIVWNGP VGVFWEAFARGTKALMDEV VKATSRGCITIIGKRSYTKLIPI

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26233	56601	A	26380	166	2172	TYILRNLYKEVMLENYRNLLSL GKAVFFPFLH*FSRDLLIT*YVP QSQQFLSQHVLIQIFLGLCAENH FHPGNSSPGHWKQQGQQYSHV SCWFENAEGQERGGGSKPWSA RTEERETSRAFPSPLQRQSASPR KGNMVVETEPSSAQRPNPVQL DKGLKELETLRFGAINCREYEP DHNLESNFITNPRTLLGKKPYIC SDCGRSFKDRSTLIRHHRIHSME KPYVCSECGRGFSQKSNLSRHQ RTHSEEKPYLCRECGQSFRSKSI LNRHQWTHSEEKPYVCSECGR GFSEKSSFIRHQRTHSGEKPYVC LECGRSFCDKSTLRKHQRIHSG EKPYYVCRECGRGFSQNSDLIKH QRTHLDEKPYVCRECGRGFCD KSTLIHERTHSGEKPYVCGECG RGFSRKSLLLVHQRTHSGEKHY VCRECRRGFSQKSNLIRHQRTH SNEKPYICRECGRGFCDKSTLIV HERTHSGEKPYVCSECGRGFSR KSLLL VHQRTHSGEKPQMTFSG VTPQLLERTVLLLAEMHSRDAL RSGTHSQPQGAACCTTGAMHLC RGTFWPQPLTQRGQLQKVIPDP EIPIELKDHVWADTLQVSFFLCP VLPSLPSESSIFCLVVCINAYAV APQSGLMREKDVHVWECGPPP FARTAPITPTSDQNWRPLREKY
26234	56602	A	26381	434	946	NTFCLTAMKILCMWFSRWHSR WVGMQGPSC*PQRTLWMATLS STGRSCVPAACTPAPCGRISAA GRLRCSQLLPHAPAPAACCSCP SVHISFQPL*QLRTSLWTVQMK SQVTQTQVGSHSSTSQARALQG HQQVQKPGSRIRTGGVKPQLEG PGRWLKIRLEGHSWTCRQ
26235	56603	A	26382	3	2119	

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26230	56598	A	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL GSSQSSRTYAGGTASATKVSAS SGATSKSSSMNPTETKAIPVSQ QMEGPHLPNKKKHKKQAVKTE PEKKSQSTKLSVVHEKKSQEGK PKEHTEPKSLPKQASDTGSNDA HNKKA VSRSAEQQPSEKSTEPK TKPQDMISAGGESVAGITAISG KPGDKKKEKKS LTPAVPVESKP DKPSGKSGMDAALDDLIDTLG GPEETEEENTTYTGPEVSDPMS STYIEELGKREVTIPPKYRELLA KKEGITGPPADSSKPIGPDDAID ALSSDFTCGSPTAAGKK\TEKEE STEVLKAQSAGTVRSAAPPQEK KRKVEKDTMSDQALEALSASL GTRQAEPELDLRSIKEVDEAKA KEEKLEKCGEDDETIPSEYRLK PATDKDGKPLLPEPEEKPKPRS ESELIDELSEDFDRSECKEKP PTEKTEESKAAAPGSCVGGCVS
26231	56599	A	26378	1	688	ITAI SGKPGDKKKEKKS LTPAVP \VES\KPDKPSGKSGMDA\ALDD LIDTLGGPEETEEENTTYTGPEV SDPMSSTYIEELGKR\EVTIPPK \YRELLAKPIGPDDAIDALSSDF TCGSPTAAGKKTEKEESTEVLK AQSAGTVRSAAPPQEKKRKVE KDTMSDQALEALSASLGTRQA EPELDLRSIKEVDEGSLPDFQQQ SLSLGLPWPKMGQFLSSTFLEG SPATQRK
26232	56600	A	26379	199	384	VYKECR*GFSHESPPSKPQS/HIE *KFCMCGENGQGLRKKSSSKN SFFGTSFTWVGRENVKHI

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26217	56585	A	26364	72	157	ERRKF**SQSS\QKKNKERLQNA VIYLEL
26218	56586	A	26365	3	620	VSGGGWEPSGTLTAFKTASAIT TEMASRS\QGIQQLLQAEKRAA EKVADARKRKARRLKQAKEEA QME\VEQYRREREHEFQSKQQA AMGFQGNLYAEVEQATRRQV QGMQSSQQRNRERVLAQLLGM VCDVRPQRPSDLQKEEMTTFSP SLIIPARACRFLVRAQQSSGHLH YRAKDPVGTRSLRHRTRSSRIHG GVPTEKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPEPIIK SLWARSDEPVFWG/LFGAGGM WSAIIAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTPSPAGDAGA CSTAGGPCQGARGPRGSGPPA WGPDAVLEPLRGQRKPYVRPM TSTWWKKLPFYRFYMLREGTA VPAVWFSIELIFGLFALKNGPEA WAGFVDFLQNPVIVIINLITLAA ALLHTKTWFELAPKAANIIVKD EKMGPPIIKSLWAPEMINPNP KRSDEPVFWGLFGAGGMWSAI IAPVMILLVGILLPLGLFPGDAL SYERVLAFQSFIGNRVFLFLMI VLPLWCGLHRMHAMHDLKI HVPAGKWWFYGLAAILTVVTL IGVCTI
26221	56589	A	26368	741	894	
26222	56590	A	26369	504	558	
26223	56591	A	26370	897	1097	RKWSQSTRLPWETGPSSETSPS GPIVSPTRSHLASPRRPPTPP*S SPRRLGAIPPGIGVPLNE
26224	56592	A	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG PTVPLVCAVCCSYWDPGVPRV VRLVVRLWPLCRCGGRSGDAS VAAAPLVCGGGI*DWDHCPFV CGPSLCALRPSCGCGSGMACRV VLLLRCLAMFAFTSFFSVTEV GKFSPFPLPEFFSGFALDLSLP
26225	56593	A	26372	196	404	
26226	56594	A	26373	1	3162	
26227	56595	C	26374	287	349	
26228	56596	B	26375	366	1637	
26229	56597	A	26376	365	604	VLAVSYPSLCLLL*KPIGPEDAI YALSSDFTCGSPTAAGRKQIRG EVCPRERCSVETCLSPNFHSLVS SFPFSLQGFK

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26213	56581	A	26360	1	1217	MQRRLKRRNAGLPCEVPGYY REDASSPLLPKYKTNFSQCLVH FFDELRRHLLVKTRHVLFIPLNH DIMQAFTLHARVIVGKVPGIFS RHPHAVLHLGHSQIGLLMEYPD ELLWECKEDALALIRRDAPMLT DFTHNLLNAPLLDKQAEWCEV FDRGRRTSLLLFEHVHAESRDR GQAMVDLLAEYEKVGQLQDCR ELPDYLPYLEYLSVLPDDQAK EGLLNVAIPILALLGGRLKQREA PWDALLDALVQLGGSSSLSDN VKKQVNSEERDDTRQALDAV WEEEQVKFIEDNATACDSSPLN QYQRRFSQDVAPQYVDISAGE GQSSFQLVSYWEKDVQTCLEFL PSGGFVVSLASGVKLQFTETD NLVKDITFFGKISTRSLKTYLKD VTEKREQSCVNLELK
26214	56582	A	26361	1	783	
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEAELC QGSTS NFLQFIHPSLLSAQTVEL GLSKFVPPKKMIITQTSHCYMTS LGILFLINILPGTTGQGESRRQEP GDFVKQDIGGLSPKHAPDIPDD STDNITIFTRILDRLLDGYDNRL RPLGLDAVTEVKTDIYVTSFGP VSDTDMEYTI DVFRQTWHDE RLKFDGPMKILPLNLLASKIW TPDTFFHNGKKSVAHNMTTPN KLLRLVDNGTLLYTMRLTIHAE CPMHLEDFPMDVHACPLKFGS YAYTTAEVVYSWTLGKNKSVE VAQDGSRLNQYDLLGHVVGTE IIRSSTGEYVVMTHFHLKRKIG YFVIQTYLPCIMTVILSQVSFWL NRESVPARTVFGVTTVLTMTTL SISARNSLPKVAYATAMDWFIA VCYAFVFSALIEFATVNYFTKR SWAWEGKKVPEALEMKKKTP AAPAKKTSTTFNIVGTTYPINL AKDTEFSTISKGAAPSASSTPTII ASPKATYVQDSPTETKTYNSVS KVDKISRIFPVLFAIFNLVYWA TYVNRSAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ ANEHPHETMSEAQPQINSATGV VKGINDLÆSKKITHHDPNIAAVN WPEMTMRFTITPQTKMSEIKTG DKVAFNFVQQGTL SLLQVIKVR KPAQ



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26206	56574	A	26353	70	745	ERGSTRVIVRASSLCPRSFQSWP PVTRASESQPLTSRQWRSDGA FKEVKLSYKGYVVLFFYP DFTFVCPTEIIAFSNRAEDFRKL GCEVLGVSVDSQFTHLAWITT PRKEG\GLGPLNIPLADVTARR\ LSEDYGVLETDEG\IAYRGLAFII DG\KGVLQRITV\NDLPVGRS\V DEALRLVQAF\QYT\DEHGEVC PAGWKPG\SDTIKPN\VDDSKEL YFSKHN
26207	56575	A	26354	1	689	MAAEDELLLPRLPMLLETGKQ LLDEVELAAETTGYYQIVQEKRA REHFNYLTQCHYYHIAKFELL KTKNNSAENHTANSSMAYPSL VAMASQRQAKIERYKQKKELD HRLSAMKSAVESGQADDEHER PPVKSFILTRNTAQAKLFGASYP SLATMTVSDWYEQHRKYGALP DQGIATATPEKFRKAAQQQKY QEVKEGEDDE/ALYRVREWDN WKDTHPGGYGNRQNMG
26208	56576	A	26355	1	810	NYLTQCHCYHVAEFELPKTMN NSAENHTANSSMAYPSLVAMA SQRQAKIQRYKQKKELEHRLSA MKSAVESGQADDERVREYYLL HLQRWIDISLEEIESIDQEIKILR ERDSSREASTSNSSRQERPPVKP FILTRNMAQAKVFGAGYPSLPT MTVSDWYEQHRKYGALPDQGI AKAASSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSS/PSSQEFR KAAQQQEEQEEKEEEDDEQTL HRAREWDDWKDTHPRGYGNR QNMG
26209	56577	A	26356	223	359	RKQQDEPCGHLQSPGKPFLTLS CRDPWGGPLPV*LEKDHRKKKS
26210	56578	A	26357	1	3855	
26211	56579	A	26358	1005	1293	SDRRYEWDP CPR*LNGALLCLL LLEHPEGCPWHSVWSTGHSLEP MHFRFPSSQDLQLLLPLPGKLG YRARIRNHGHSCLQRKRTVYQ GDGPLREP
26212	56580	A	26359	763	978	

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26204	56572	A	26351	3	2212	MKRSRCRDRPQPPPPDRREDGV QRAAELSQSLPPRRRAPPGRQR LEERTGPAGPEGKEQPPALASQ SAEIAASARLPPRLGRLLGFQK ACRCWSLNPILMALLRSLVPP DKKHPQVWRGRPPLHLAPNVG LFSRVKVRSSVVEDKSMRDSR RGLSQRRRRRKKKKRGSSSKK KKRRKKRKKKKRKKRKRKN RKKKKKKRKNKRKKKRKKEEK KEEEEERRKKEEDEEGRGRGR RKRRKKRKKRRSRKKKETAA AAAAGERLGKWWPGECVPEC VAYFLRRRLQQLHPARQLLL QGMAGYLSEDFVMVEEGFST RDLLKELTLGASQATTDEVAAF FVADLGAIVRKHFCLKCLPRV RPFYAVKCNSSPGVLKVLQAL GLGFSCANKAEMELVQHIGIPA SKIICANPCKQISQIKYAAKHGI QLLSFDNEMELAKVVKSHPSA NFHIGSGCPDQAYAQSIANAR LVFEMGTELGHKMHVLDLGGG FPGTEGAKVRFEIIVINSAL DLYFPEGCGVDIFAEGLRYVV TSAFTVAVSIIAKKEVLLDQGR EEENGSTSKTIVYHLDEGVYGF NSVLFDNICPTILQKSSTKSLR TTIGEAFERLHRLLRERQKAML EELEADTARTLTDIEQKVQRYS QQLRKVQEGAQILQERLAETDR HTFLAGVASLSERLKGKIHTN
26205	56573	A	26352	1	860	MKKEDAFKAFYIVHGKWNCV KGSLTRTPCCCTNCLAGGIWC MRVQIFQLENKVLPGFPWACR VDLYGQIGFDAAAQCLSLSVSK AEPLVKKAPPELREQRLARKTSL SDNLKYLFDNKDIMKVQSKK KKEHSFRKNNGCIKIIAFSDHAE DFRKLGCSEVLGISVDSQFTHLA WINNPQREGDLGPLNIPLAEV ASGLSEDYAVLKTADAGIAYRG RFISDGKGVLSQITVNDLPVGR SVDEALRLVQAFQYAEHAEV CPAGWKPGTDTIKLNVGDSKE

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26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTSGPGSSQ*LTGSPQECC TPAGETGPRAHSPQ*SCWCHCC TPQGRQSICTRTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMHSKRCAGGKIRVGTPE CQ*SALERPGLPLC
26199	56567	A	26346	368	746	SLLHTTSRAPEGPSRYPGPGPPS AATKGQRRRPLCARPP/PGLPD APL/SPAAPTPTLPLCPRVAQP AHGPPSASALSSWENRPCCRHE LAAKPPEQAARRGHARTPTAG PAPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRGGFGRVTGQ*WRE GQQINK
26201	56569	A	26348	1	3369	
26202	56570	A	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHLSCLSLKFGVSLKSCRIT LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFPGTE GAKVRFEIASVINSALDLYFPE GCGVDIFAELGRYYVTSFTVA VSIIAKKEVLLDQPGMEEENS
26203	56571	A	26350	146	502	

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26190	56558	A	26337	1	1316	MNGLLDSDSDSLSSCQQRVKA RLHEILQKDRDFTAEDYEKVES RIYHFARLSVGGYTADSSLTLK VYLQLMKAPKKRRGEVNVGT VVAFIKGGFPVVKKDYFRPAA DGSSALCRFFPTGNVHDQSDPQ KVTDGAVVPVQPTDGPGLRCL RRARGCGAGRQGREQAQDCG AEIQAEAASRASRVQEGSYPRP PNGPFSTDLTGLMQFTKLLVLK VESQLTRRIRKCHNLREANHREE LRRFNCTNVALRTGVQFNRRPD SPGYSRGVLSPERHVRTRL YFT SESHVHSLLSILRYGALCNRRG TLCCRAIHTLHRHTIVLNGVT TLNLVQLTFYGNVSEIIRHQCQ LTRHGNHPLPLTAIQGIALFSDN QAAYRFRADQRTLRFGLPVAR QPVRRGGFHDIIVFDGTARQ QQE/LRLQLRVFSSFVLHEKKR
26191	56559	A	26338	2	1415	
26192	56560	A	26339	1434	1667	KRTDWRDRVAFRCRSIAESG*R QAIAKELELTASAEILLWDDYF APGYGVPNDEGMEAVKLLARL EGILLDPAVRLR
26193	56561	A	26340	1	1671	
26194	56562	A	26341	1067	3947	FCTVPNAVYIGGPGFGARHNAS NSLKDIAELVPFAHRYGAKIFV TLNTILHDDELEPAQRLITDLYQ TGVDALIVQDMGILELDIPPIEL HASTQCDIRTVEKAKFLSDVGF TQIVLARELNLDQIRAIHQATD ATIEFFIHGALCVA YSGQCYISH AQGRSANRGDCSQACRLPYT LKDDQGRVVSYEKHL LSKMDN DQTANLGALIDAGVRSFKIEGR YKDMSYVKNITAHYRQMLDAI IEERGD LARASSG
26195	56563	A	26342	182	881	HAELPYRGLLLKLGESRGCLL PASLPFSLQEFFYSGPREELAQK TLLVSVWDYDLGTADDFIGGK CDPADQDVVHTALREVTREELG LAVPEEHVWGLLRPVYDPQKA TVVPVLAVGGLDPQSLRPNSE EVDEVFALPLAHL LQTQNGY THFCRGGHFRYTLPVFLHGPHR VWGLTAVITEFALQLLAPGTYQ PRLAGLTCSGAEGLARPKQPLA SPCQASSTPGLNKGL
26196	56564	A	26343	237	338	

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26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH NFVCTAADTFTTDITPKAGDAR LIGIAQTVRHLEDPMRAWKSIH KSCEILDPIHRAPVKENTHPARK INISDPAAGAVARIRYEGVLSVC RASASAYVSRRTITVACWYVS NTGVTGATIGVKRQHRHARLFS GDGAPGFGTGKRDRLRRLVR IQIQRFTFAAVLHVPTPWSRAID AAALLTVIDVKVLTACACQAC RTLALRVAQVIDRCSNPGDIMS SVARRYWFISRWSAKRDCAVS YDQDPGQAQRSCRSCLVAVDR GLWLSAYCRSLMTQTLLPDDV PRILPNASSPSRLRCLQHLGNYR LLDLRKLWLHRSQFSLCGWEK RLVKDLTRIQDTGRAKEILGAT ATLEFRLVNTNVDQAAAASGR VPGDSEVKQTREGQPVVLYKR VILTDGHDSTSSQDEYNQPP VNISLDSAGGNIMSNFTKDNIG KPMATLFVEYKDSGKWDANG RAVLVKQEEVHIANIQSRLGNS FRITGINNPNEARQLSLLLRAGA LIAPIQIVEERTIGPTLGMQNIEQ GLEACLAGLLVSILFMIIFYKKF GLIATSALIANLILIVGIMSLLPG ATLSMPGIAGIVLTLAVAVDAN VLINERIKEELSNGRTVQQAIDE GYRGAFSSIFDANITTLIKVIILY AVGTGAIKGFAITTGIGVATSM FTAIVGTRAIVNLLYGGKRVKK
26189	56557	A	26336	1	369	

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26183	56551	A	26330	34	1949	MGYLNNAVAGYREDLLANRAIV KHGNFALLTPDGVVKNIPGYE NCDATILSTPKLGASFVDYLV LHQNGGNQQGFGVEGIETFRY VISGNITAKAEGKTYALSEGGY LYCPPGSLMTFVNAQAEDSQIF LYKRRYVPVEGYAPWLVSNA SELERIHYEGMDDVILLDFLPKE LGFDMMNHILSFAPGANHGYIE THVQEHGGATQAFKENNHK AYKDTYGVSHITRHDMLQIPKQ QQYEKYQDTHDTPYCEPLPGET RLWGD TDVIGL FDAETDMNDV VAILENHPLL GAGFAHKIEQLE DKDWEREWMDNFHPMRFGER LWICPSWRDVPDENA VNVMLD PGLAFGTGTIQTLSVPAMLDSS THTRMRSTLNLYEITRMSTVS TSEHSMTYTLVQVDMKEA QKP DTASYRTFNEFFVRPLRDEV RPI DTPNVLVMPADGVISQLGKIE EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVT TYLSPRD YHRVHMP CNGILREMIYVPGD LFSVNHLTAQNVPNLFARNERV ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDES FVVG GPVG DFELL LCHGTVCVVGKMRDLIL QLSKSSIYSTKPPSRQVSVM LC
26184	56552	A	26331	1	145	LRLGLLYGRRFVPPP*YALLNK DSSPWYPFSVPVLASKTRYLWL LSPT
26185	56553	B	26332	1	3090	
26186	56554	A	26333	3	832	
26187	56555	A	26334	1	3258	

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26179	56547	A	26326	2	223	RIPIKNIESAKGLDVWDSWPLQ NADRTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNSID SWKNAGR VF KDSDKFDANDPI LKDQTQEWSGSATFTSDGKIRL FYTDYSGKHYGKQSLTTAQVN VSKSDDTLKINGVEDHKTIFDG DGKTYQNVQQFIDEGNYTSGD NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDA/G*HI NLHVLSKGRRQLNRQLEKRG
26180	56548	A	26327	1	803	MLEDPRKGLETPSPVSHNLHFQ FHLGPLPGSPMKKWPALVVT GSKSPKLESYKHFQKIWDMHG EPSKREEGAGLTVNQHIPNGAS TCNEGPQRLEALGARIPMAAGF SSSKPTLVTPRRAYRADLRLEG YWGCQGVPGGPLVAQGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDA/G*HINLHVLSKGRRQ LNRQLEKRGPC
26181	56549	A	26328	2	439	
26182	56550	A	26329	1	1084	MVIAAMETQLSNGPTCNNTAN GPTTINNNCSPPVDSGNTEDSK TNLIVNYLPQNMTQEELKSLFG SIGEIESCKLVRDKITGGATQAF AKENNQKAYKETYGVSHITRH DMLQIPKQQNEKYQCDNLKT CHTSHGSVMAETAVINHKKRK NSPRIVQSNDLTEAAYSLSRDQ KRMLYLFVDQIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTPERR**HINLHVLSKG RRQLNRQLEKRGPC

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26174	56542	A	26321	402	1781	QRTTGAERYVPHHQPCPPASSL SAGPRGLHPAKVQEGVDIAIEN DVIVAIGDALQTQRYPDASFKEM HGRIVMPGIVCSHNFYSGLSR GIMANIAPCPDFISTLKNLWWR LDRALDEESLYYSGLICSLAIAK SGCTSVIDHHASPAYIGGSLSTL RDAFLKVGLRAMTCFETTDNRN NGIKELQEGVEENIRFARLIDEA KKATSEPYLVEAHIGAHAPFTV PDAGLEMLREAVKATGRGEHI HAAEDLYDVSYSHHWYGKDL LARLAQFDLIDSKTLVAHGLYL SKDDITLLNQDAFLVHNARSN MNNHVGYNHHLSDIRNLALGT DGIGSDMFEEMKFAFFKHRDA GGPLWPDSFAKALTNGNELMS RNFGAKFGLLEAGYKADLTICD YNSPTLLADNIAGHIAFGMGS GSVHSMVMVNGVMVYEDRQFN FDCDSIYAQARKAAASMWRRM
26175	56543	A	26322	284	340	
26176	56544	A	26323	113	646	WTLVPNWNNTQPYLGLFF*FIR DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQRSDSSLR EKKITKKHTKKRTASLILHAMI CCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ
26177	56545	A	26324	1	582	
26178	56546	A	26325	3	947	QTQEWSGSATFTSDGKIRLFYT DYSGKHYGKQSLTTAQVNVSK SDDTLKINGVEDHKTIFDGDGK TYQNVQQFIDEGNYTSGDNHT LRDPHYVEDKGHKYLVFEANT GTENGYQGEESLFNKAYYGGG TNFFRKESQKLQQSAAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGGATQA FAKENNQKAYKETYGVSHITR HDMLQIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQ NADGTVAEYNGYHVVFALAGS PKDA/G*HINLHVLSK



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26164	56532	A	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDHK RPREALLDSLKKLQLDYIDL MHWPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQQ GKGVFDQKVIRDLADKYGKTP AQIVIRWHLDSGLVVIPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDQFGG
26165	56533	A	26312	3	793	
26166	56534	A	26313	181	336	
26167	56535	B	26314	1	374	
26168	56536	A	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG RNSKRLIALISAIGMSIFLQNYV SLTEGSRDVAPSSVPLTPASLLI AGSPPH*TISRLSGPLLREIMLK QLYHCGKSLTNLPIREILRM*G* LTGEEIELARGDFHIRDIWHRA VTNTAHKTGITQAQHRH
26170	56538	A	26317	627	878	VVEWFEPLICVNGWESKWPVL LSE**PETVGTNCDSSN*IPASLN TSYTGLMAFDAMVAVPTS*TC KIRRRVAGTKCGNPRA
26171	56539	A	26318	125	3078	IYTVEIQNLGFAFVTGENTTGIN SGTISLLQNGKDPAPSPIVLLAT NGGSATNAGTITGKVTEQHSVF NKYSTGTSNSFIFNNDVSSITGL VAQSNSTIINTDSGIIDLGRGS VGMLAIADSTAENQGKITLDSM WVDANDTTAMRDIASNSAIDF GTGVGVGTDRYRGGRKNAPAF NQLGGVITIYNAGAGMAAYG ASNTVINQGTINLEKNGNYDDS LAANTLVGMAVYEHGTAINDQ TGVININVGTGQA
26172	56540	A	26319	205	419	
26173	56541	A	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK CTAGRRSQQFSARSTLKPMPS R*SSMHR**MPSASCALRLPIP PAAAQSSHQSKKLRTSDNASPV AAARPVRPIRWT

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26154	56522	A	26301	2	1021	TPGNNVDSIFLAFFLNQFLTGLGY IMGKTISIKVLFGIYLLLMAAKV FAFSCNVDCGGINAGTTSVYV NLDPVIQPGQN LGVDLAHHISC WNGDGGWYDTDHMLVQGS AFAGSLQSYIGSLYWNNTYYPF PLTTNTNVL DIGDKTPMPLPFK LYITPVGAAGGVVIKAGEVIARI DMYKIATLGSGNPSNFTWNIIT NNNAVMP TGGCTVDSRNVTVD LPDFPGSAEIP LGVYCSSEKLS FYLSGATTSSRQVFANTAPDA TKASGVGV TLMQRQLAGINDS HLLHYLDDEVWDNDYLATPHF LLKSAILRSMNDALMTRVTGE KNGQVRLEEIER
26155	56523	A	26302	522	714	
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPILPNYVA TAVAARIADVQGISDTCVIAQP SPPHPGALRTLVTFTDEPETPQP PGAAGFQLVQKKQVQLHNVLY VMTPHAFAGQTVTIYLPGEQQT LSVAPLKNVVQLVTQQHLRDR LWWPGAFLTDFAAKV KALKD/ YPNHVMAQRASGEAEADDV AATIKSVRQQLNLNITGRLPV KLDPDFVRVDENSNPLVGDYT LYTVQRPGTEQGSFKVKRARA RVRQTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAARILIAE EQSREVKIALVVLDR LQRE
26157	56525	A	26304	1	1701	
26158	56526	A	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR WRDPYDHYPARPAYCP*R/WC M*LSTLATPKKVSPCKPAPAAH RWR
26159	56527	A	26306	1	3270	
26160	56528	A	26307	1962	2049	
26161	56529	A	26308	94	942	
26162	56530	A	26309	1	4104	
26163	56531	A	26310	879	1367	TASELGKSCSRDHTPCTASVRA LYYARLRHAPANDPGEDGWAL AAKPPALPPRNSLNSQAIFRDKP NLPHRSPATYRQTERG*DTRSE FHA*TD AIPVATRARAGEFCRQ MFWGEDQADEQPA**ACCHRK *PVPK*DLAMLRAPPRMDSPPD ASRTSDLHN

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26152	56520	A	26299	1001	2193	LMAATKPAFNPPGKKGDIIFSV LVKLAALIVLLMLGGIIVSLIIS WPSIQKFGLAFLWTKEDAPN DIYGALVPIYGTLVTSFIALLIA VPVSFGIALFLTELAPGWLKR LGIAIELLAAPSIVYGMWGLFIF APLFAVYFQEPVGNIMSNIPV ALFSGPAFGIGILAAGVILAIMII PYIAAVMRDVFEQTPVMMKES AYGIGCTTWEVIWRIVLPFTKN GVIGGIMLGLGRALGETMAVTF IIGNTYQLDSASLYMPGNSITSA LANEFAEAESGLHVAALMELG LILFVITFIVLAASKFMIMRRIA LTLSMATMAFGLFWLIWILMST ITRGIDGMSLALFTEMTPPPNT GGGLANALAGSGLLILWATVY CGPLSDDRGGIRPTI
26153	56521	A	26300	1	1645	MPAPPYTADYFSGLTATTAALA ALHKVRETGKGESIDIAMYEV MLRMGQYFMMDYFNGGEMCP RMSKGGKDPYYAGCGLYQCAD GLLSLDCVHRRLLGAIDPILNECF KDIGLAHLLGTPEIPEGTQLIHRI ECPYGPLVEEKLDWLATHTIA EVKERFAELNIACAKVLTVP ESNPQYVARESITQWQTMMDGR TCKGPNIMPKFKNPQGQIWRG MPSHGMDTAAILKNIGYSENDI QELRPPNNKRTKMDRGAMDII GGQHLRQMWDLDADVYGHKT ALICSSGGVVNRYSYLELNQEI NRTANLFYTLGIRKGDKVALHL DNCPEFIFCWFLAKIGAIMHE AVIALASPDNMNAFELTP*SGK LITTFPHLPLAISA*ASPACSEK RWVMALRGHSFQSVRSWAHFS IWNRLVTQEPIRR

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26148	56516	A	26295	1	1848	MDLSTPERGSPYPRLLPCGDPL GETIVAIDQEAKPSTEDLGNNK ETKYIKLKVIRWDNSDFNLYS NYERIRARTTKKEDSATNVPVT FEKHGSHAVVYARRSATVLT RNKEAPRVPQGGYMVSFVDIPE ALTQGETVAEAMEAAKDALLT AFDFYFEDNELIPLPSPLNSHDH FIEVPLSVASKVLLLNAFLQSEI TQQELARRIGKPKQEITRLFNH HATKIDAVQLAAKALGKELSLE CLMDILNLNKHISGQFNAELES RTQVMTLGGMVDPKQLSDAITA IHNQDSDLAKRVIEGHKNLNM MEVAIDEAR/C*AIIAKHQS/TAS DLRLVMVI/SKTIAEMERIG/DV GRNKICRTALEKLSQQHQ*VV S/LE\SLDRHTIQMLHDVVKAF RMDIDETAKCQIFVEYVLKPKV IWLLCFANIFLYVVRIGIDQWST VYAFQELKLFKAVAIQGFTLFE AGALVGTLLWGWLSDLANGR RGLVACIALALIIATLG VYQHA SNEYIYLASLFALGFLVFGPQLL IGVAAVGFVPKKAIGAADGIKG TFAYLIGDSFAKLGLGMIADGT PVFGLTGWAGTFAALDIAAIGC ICLMAIVAVMEERKSAARKKFS
26149	56517	A	26296	395	1428	TSATATSTFALPRGGGYLVVSE WVVLRFDTDFLRIFPCDNGRTILI RFGIFRMLMIVAIETQQFPVTAI FRVIGMVVINNVNASEETNRRL HHRSLRLIQECVMDSLNLNKHI SGQFNAELESIRTQVMTMGGM VEQQLSDAITAMHNQDSDLAK RVIEGDKNVNMEVAIDEACV RIIAKRQPTASDLRLVMVISKTI AELERIGDVADKICRTALEKFS QQHQPLLVSLES/LGRHTIQMLH DVLDAFPRMDIDEAVRIYREDK KVDH/EYE\GIVRQLMTYMMED SRTIPSVLTALFCARSIERIGDRC QNICEFIFYVKGQDFRHVGGD ELDKLLAGKDSK
26150	56518	A	26297	667	1002	
26151	56519	B	26298	1	1716	

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26143	56511	A	26290	1	1817	MTSAISLGSRCGRIPSDIIGSNL DITAFNWQPDLLTIWHRQLHLH LTRLDGGGHFYRQEVHLWRD KSGDKRRPQGDPKTTGITAKVI NVRSTKL VGLPHRITATRWKR KRSRMLHTNTGKLVFNNRDQK RCTRKVMFDKALKLLDEAERL GSTSARSTIYQQCKRQGVITPHS ADFATTVRLLAHLSQERLGKLQ DSIYISLTDHCQFAIKRFQQNVL LPNPLLWDIQRLYPKEFQLGEE ALTIIDKRLGVQLPKDEVGFIA MHLVSAQMSGNMEDVAGVTQ LMREMLQLIKFQFSLNYQESL SYQRLVPHLKFLSWRILEHASI NDSDESLQQAVKQNYPPAWQ CAERIAFIGLQYQQGLTQPAV SKIINDIEDYFGVELVVRKNTG VTLTPAGQLLSRSESITREMK NMVNEISGEKNPGEGSEKELET VYVQAVGAHWEGNQVWLILA GGALFAAWPRVYAAAFSGFYV AMILVLCSLFFRPLAFDYRGKIA DARWRKMWDAGLVIGSLVPPV VFGIAFGNLLGVPPFAFTPQLR VEYLGSFWQLLTPFPLLCGLLS LGMVILQGGVWLQLKTVGVIIH LRSRVRIPCDLHIYAQMA
26144	56512	A	26291	557	808	
26145	56513	A	26292	8	274	
26146	56514	A	26293	523	1851	
26147	56515	A	26294	1	589	

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26138	56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLEGM MPMRNIIKLALAGLLSVSTFAD AAESSPEALRIGYQKGSIGMVL AKSHQLLEKRYPEKISWVEFP AGPQMLEALNVGSIDLGSTGDI PPIFAQAAGADLVYVGVEPPKP KAERILVAENSPIKTRTDLKGH KGAFQKGFSSHNLLLRALRQA\ GLKFTDIQPTYLEPRWRPRAA\ FQTRGTVDAWAIWDPYYSAA LLQGGVRVLKDGTDLNQTGSF YLAARPYAEKNGAFIQGVLATF SEADALTRSQREQSIALLAKTM GLPAPVIASYLDHRPPTTIKPVN AEVAALQQQTADLFYENRLHY SEYCRPMVSVGNWFLDGSHSV FSYDALDRLVQQGGFDGRTQR YHYDLTGKLTQKQWQYDGHG WLTDISHLSEGHRVAVHYGYD DKGRLTGECQTVENPETGELL WQHETKHAYNEQGLANRVTP DSLPPVEWLTYGSGYLAGMKL GGTPLVEYTRDRLHRETVRSFG SMAGSNAAYEMTSGETELIDLC
26139	56507	A	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH LICFTSPVNTFLRYNAFTLCNGE FGMSHPALTQLRALRYCKEIPA LDPQLLDWLLLEDSTMTKRFEQ QGKTVSVTMIREGFVEQNEIPE ELPLLPKESRYWLREIL\LCADG EPRLAGRTVVPVSTLSGPALAL QKLGKTPLGRYLFTSSTLTRDFI EIGRDAGLWGRRSRLRLSGKPL LLTEFLPASPLY
26140	56508	B	26287	184	415	
26141	56509	A	26288	15	87	
26142	56510	A	26289	78	157	CKRYGKARDTG*QPRTQKCTC CELDE

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26135	56503	A	26282	1	1338	MTRHYGAEATNALLPGKASKH QIVGCGVNALSDLPDRPDKTR SVASGIGAALLRLIKTLADDL QNLTDLSVFNGERYKDAQHV IRAAGEKNQAFIAGARHDLGGE LGVGLVWIPASKVNGIMGPSPV WLTRVSNIAGESAEGLLVTKP KNYDQVPANKPIVDAIKAKKQ DPSGAFVWTTYAALQSLQAGL NQSDDPAEIAKYLKANSVDTV MGPLTWDEKGD LKGFEGVFD WHANGTATDAKRYCANVKGV NPDTQEPSPSGVKVNDPKVDER LIRQEAGMVFFQFYLFPHLTAL ENVMFGPLRVRGANKEEA EKL ARELLAKVGLAERAAHHYPSELS GGQQQRVAIARALAVKPKMM LFDDPTSALDPELRHEVLKVMQ DLAEEGTMVIVTHEIGFAEKV RSRLIFIDKGRIAEDGNPQVLIK NPPSQRLQEFLQHVS
26136	56504	A	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS ADPAGDIPPIFAQAAGADLVY VGVEPPKPKAEVILVAEYSPIKT VADLGCPLHVQKVSRYPPFTQ VITPVQCYVTIDALGQYAAWT RANMTYRPGSNIIQNLGNDIRL RTVQ
26137	56505	A	26284	3	1351	RTAPETPNQRPATLDSGILGGYI APDNLTITFIGGHS LFDERFCLA HRCQKAAEDDAFPDSDLDAAS LLEYAREKLNGLDVEVYHWNL QNFAPEDLLYARFDSPALKTFT EQLQQADGLIVATPVYKAAYS GALKTLDDLPERALQGKVVL P LATGGTVAHLLAVDYALKPVL SALKAQEILHGVFADDSQVIDY HHRPQFTPNLQTRLDTALETFW QALHRRDVQVPDLLSLRAPKP KAEVILVAENSPIKTVADLKGH K/VAFQKGS/SSHNL LRA/LRQ AGLKFTDIQPTYLTPADARA AF QQGNVDAWAIWDPYYSALL QGGVRVLKDGTDLNQTGSFY L AARPYAEKNGAFIQGVLATFSE ADALTRSQREQSIALLAKTMGL PAPVIASYL DHRPPTTIKPVNAE VAALQQQTADLFYENRLVPKK VDIRQRIWQPTQLEGKQL

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26126	56494	A	26273	1	1038	MGCLDLGDGRAGSVARYFRRY RPPCDAALDLAKGVDVMVHEA TLDITMEAKANSRGHSSTRQVL KKILFGLEPYEISTLFEQRQAML QSIKERSRRHRLPKEKKIMTPTI ELICGHSRIRHFTDEPISEAQRE AIINSARATSSSSFLQCSSIIITD KALREELVTLTGGQKHVAQAA EFWVFCADFNRLQICPDAQLG LAEQLLLGVVDTAMMAQNALI AAESLGLGGVYIGALRNNIEAV TKLLKLPQHVLPLFGLCLGWPA DNPDLKPR\LPASILVHENSYP LDKAALAQYDEQLAEYYLTRG SNNRRDTWSDHIRRTIIKESRPFI LDYLHKQGWATR
26127	56495	A	26274	1	1338	
26128	56496	A	26275	2	375	HSDPEASGPLTRLRAMEQRRVT DFFARRRTPGSVPSTDRR*TIVR MIPCTSSGRRTKAMVILRTSLV NPASNE/CATELFNALDVSIQNP RMIISP*IQHRTLSGSPLVAVG RMCSLTPRVIFEH
26129	56497	A	26276	219	767	RFTQGGKGPINPAVIRPLDFPQN GSRPLANQ\FTTSLKVGDFYFGK RHKDVLRAIRNLKCSDDFTQRN FAPIDFIDKNGDVQPMYNITRD GCMMLVMGFTGKTAAAVKEC YINAFNWMAEQLNRRMAMGE ELQHRYAIKETRSKLKGTIGTR LMNERKKEKRVLELEHEHIMQ VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR PAGFLDG
26131	56499	A	26278	3	399	
26132	56500	A	26279	1112	1831	TGIRNCAPLSLTWKSKTANRKV RCGHIRYPLADGAKTSDGKDY LVVATTRPETLLGDTGRSRLTR KIRVTKELIGKYVILPAGTAPGV RQGPVWMPGDEVKKVTCKNG VVNEIWTRNHADIPLRPRFAVL ASGSFFSVGLVAERNGIREPILG LDVLQTATRGEWYKGDFFAPQ PWQQFGVTTDET/LRPSQAGQT IENLFAIGSVLGGFDPIAQCGG GVCAVSALHAAQQIAQRAGGQ
26133	56501	A	26280	3	790	
26134	56502	A	26281	334	609	



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26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIQAIAEAVR KRNDLLFIVVTDMQSLRYSHPE AQRIGQPFGDDILKALNGEEN VAINRGFLAQUALRVFTPIYDEN HKQIGVINDSRWSIIWSVLFGM LVGLIGTCILVKVLKKILFGLEP YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTPRRDEEITIKDRLL LINTVPRVSRNGVIIAISTFRDKT EVRKLMQRLDGLV/NLC*RTS* TIPLRAHSPQSKSAIYHEIAP*NA PAFYRRKCHCADIFLPYF*TCR\ RDRAMSAYLRYIVQKADSSFL YDKYQNSIAAHVMRALAAEQ SEVSPEQRRACEAFESANNTH GLNLTAHKYPGLRGTLQTAST DCDTIVEAAALLPAFDQAVEGN RHQDDYGSGLGMAEEKFHYYL DLFRAVG DGHNSKEDATFGLG WRVNGNATMTPTFGTLASPQT YGHTGWTGTVTVIDPVNHMTI VMLSNKPHSPVADPQKNPNMF ESGQLPIATYGWVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI TPLLRGTGLISNSRSLIVISSR RGVPSRNTSETSTTCDEWLSV DSFSIVLRLTVIQQLCGIVDQR DLAAIVHGND AFFDRLQHGLA LLKQRGDFVGFQAEKDFQYL NQNAGANQSDQHAK*Y/LTR*C SSDCH*SVGSHGLTQGRSPPRQ FVYDFHRRWG
26125	56493	A	26272	1	2700	

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26120	56488	A	26267	1	1657	MLIQRRRLAFDRAKHRRRAEML AQRARGEESAAHHSSPEGAIEV DESEVDLDAISAQSLRLVRSILM LIALLSVIVLWSEIHSAFGFLENI SLWDVTSTVQGVESLEPITLGA VLIAILVFIITTQLVRNLPALLEL AILQHLDLTPGTGYAITTITKYL LMLIGGLVGFSMIGIEWSKLQW LVAALGVGLGFGLEIFANFIS GLIILFEKPIRIGDVTIIRDLTGS VTKINTRCHTHRRQQLLLQQA ATSSADVIYLGEAVCSKRRATK VGDWLEMAKSLAGSGKQIVLS TLALVQASSELGELKRYVENGE FLIEASDLGVVNMCAERKLPFV AGHALNCYNAPLKKILLKQGM MRWCMPVELSRAWLVNLLNQ CDELGIRNQFEVEVLSYGHPL AYSARCFTARSEDPRKDECETC CIKYPNGRNVLSQENQQVFVLN GIQTMSGYVYNLGNELASMQG LVDVRLSPQGTDTFAMLDFA RVNENGAAPLPLTANSDCNGY WRRLAGLSLRQIKTCLIFLLCQP RGRRPYRTRAMPPIITMPANSP
26121	56489	A	26268	482	605	
26122	56490	A	26269	1	298	MWPGMVTHAVRIPLHNDTVTL SDNFQPFAGTDAMTITRPLEML RDGKCPQPDWISSEGACAGNA TDSPPFELKAGKTITLEDGRQI NGADYLAAPVPGKALAIFGDT GPCDAALDLAKGVDVMVHEA TLDITMEAKANSRGHSSTRQAA TRESELFRTYVKHSLIFASVIGII TLLQASTKIYTPGRKEQGEPMT PRRTPARF*IKSGQNNHAGRWK AD*RRLLSCSSAR

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26113	56481	A	26260	301	1313	RLEHDGVCLHRANHRYPGCRL HLDYVEPQLQHDDALRAAVM MFKQYLQVTKPGIIFGNLISVIG GILLASKGSIDYPLVIYTLVGVS LVVASGCVFNYYIDRDIDRKME RTKNRVLVKGLISPAVSLVYAT LLGIAGFMLLWFGANPLACWL GVMGFVVYVGVSLYMKRHS VYGTIGSLSGAAPPVIGYCAV TGEFDSNAAILLAIFSLWQMPH SYAIAIFRFKDYQAANIPVLPVV KGISVAKNHITLYIIAFAVATLM LSLGGYAGYKYLVVAAAVSV WWLGMALRGYKVADDRIWAA QSCSGFSIIPITALSVMMMSVDFM VPDSHTLLAAVW
26114	56482	A	26261	3631	4078	CFLNFKTLLLVHLFRRVFLRIRL RHRKLHPVGLGGPVNKAAYAF CLGAMANGVYGPYAIFASVKM VSAFTVTASTMLAPR\WLLGLA GITEGAIPMAIEDPLRVIGSFVL GSMVTGAIVGAMNIINRTLRE ASVTSQIVQTIIRLR
26115	56483	A	26262	814	2126	CTGCRKQRLPVVQGFAGLAA NMIGSGFLGAVVGGLIAGYLM RWVKNHLRLSSKFNGFLTFFYL YPVLGTLGAGSLMLFVVGEPV AWINNSLTAWLNGLSGSNALL LGAILGFMCSFDLGGPVNKA YAFCLGAMANGVYGPYAIFAS VKMVSAFTVTASTMLAPRLFK EFEIETGESTLLLGLADITEGAIP MAIEDPLRVIGSFVLGSMVTGA IVGAMNIGLSTPGAGIFSLFLH DNGAGGVMAAIGWFGAALVG AAISEGKRIFRYRDLIIVNSNQL FLHDHRFPRWEGLESVFFLLAA FQQDVGIWPPLGAMLGLATAV VLGFLLYWGGIRLNLGAFFKW TSLFILVAAGLAAGAIRAFHEA GLWNHFQEIAFDMSAVLSTHSL FGTLMGIFGYQEAPSVSEVAV WFIYLIPALVAFALPPRAGATAS
26116	56484	A	26263	1	525	
26117	56485	A	26264	1	700	
26118	56486	A	26265	1	1428	
26119	56487	A	26266	254	475	RDQLVSELNQMLV*KSAFRMA ALITSRWPMVTHWFREVRRGN WRQFLPALTLVRLSLMLMGR QAILRSRRNY

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26111	56479	A	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS LTLHQDPVYVTRADAPVAGKV ALLSGGGTEHEPMHCGYIGQG MLSGACPGEIFTSPTPKIFECA MQVDGGEGVLLIHKNYTGDILN FETATELLHDSGVKVTTVVIDD DVAVKDSLYTAGRRGVANTVL IEKLVGAAAERGDSDLACAELG RKLNNQGHSIGIALGACTVRS GKPSFTLADNEMEFVGIHAIL KGDIPAEAILASIKPAGVVSRA DVVLPNQFQALRKSFIPERPVP VMVTRLFELPVQISLGVYSLER PANPQPIAYLVLPQRRKANNQN ASTSAIIRATIGEPISCSVPSRGC EGGISVAETVPAMIIAIGITISEG LDARYRHVNSEHDPSDRQAKF EWRYFGNLGKTVNDWRKNNK ADIKEDGNRRCRHTNQPHCRIE AVEYDDGRLCPLHGAHRGQSS DGELVKPTVKTQSLAVHYSIGK LRHRPNHGAVYYQRLRSGMGL MNAFDSQTEDSSPAIGRNLSR LARKKLSEMVEEELEQMIRRE FGEQEQLPSERELMAFFNVGRL RAGSVKTKRSGANKQRRTRCV SRPSADTIIGELSGMAKDFLSHP GGIAHFEQLRLFFESSLVRYAA EHATDSRDPRYRPFYSISRVP VSDNITLQQLLSLNDQPARCK PSARCRLHGSHTSRYECNHRHG
26112	56480	A	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS LIRCTTRFSSQLSLGIATMSHRK RVISALKSLSRLSANSLVFANQ VERSSLTNLGCTRCSG*SLFWQ RPALR*PFGLCPTVALTYLIVSP EW*KAVSVKCVWRNRRLTLMTS PICTNSGTLTTAPVDRVAQVTF QSPECLQHMRLTIALRYFRVAL SRLLLVYASVCFTFSG

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26103	56471	A	26250	2	563	STTSSTTAFSATTAGTPSTGNTP SASPIWRRPNFWARKVYLLHW FCHRQPSKEVLFHLALYRNNPR CKAVVHLHSTWSTALSCLQGL DSSNVIRPFTPYVVMRMGNVPL VPYYRPGDKRIAQDLAERETH\NHAFLLANHGPVVCGESLQEA ANNMEELEETAKLIFILGDRPIR YLTAGEIAELRS
26104	56472	A	26251	2	1481	PENQINKLKQAIPADYRSHQKC VNQPSSPTITPRLFAITVITDERG YATGSAGNLSL/LLPDGNLLAT PT/GSCLGN/LDPQRFSKVAADG EWL/SGDKPSK/EVLFHLALYR/ NNPRCKAVVHL/HSTWST/ALS CLQGLDSSNVIRPF/TPYVVMR MGNVPLDLAELAA/DNQAFL LANHGPVVCGE/SLQEAANNME ELEETAK/LIFILGDRPIRYLTAG VCPLAKMLNGTGQYLSIKRCT NNRSVRGTCSAPRAGPKGYGL MMMIDVLSASYSAYRSGDRTL LYSYHRASACADSTTLTVLISY TFHLVNSYSTVPPLESGTQPA SPSFPTRVSDDHNRDFFLLSPC GLLQNLAQCIRQVGIQLDFGCV IISAQTETDGPLVCGRFEEGTPF SPQTPRDCDPNRSYSGNTQGVR GATSSPGSAISFEQTVNARSHVL RVTLTLGLTRPMLYVTGSLKWI NICILPISLKPLRYIHLAAQFPT APISLGRSLHVPHEEVAM
26105	56473	A	26252	1	413	
26106	56474	A	26253	3	247	
26107	56475	A	26254	300	665	
26108	56476	A	26255	1	1854	
26109	56477	A	26256	1	1611	
26110	56478	A	26257	942	1040	

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26099	56467	A	26246	1	2625	MVAFYRHAGRMWPGIALSCSL GNIAASILLFSTSSLNMTWTTINI VEAVVGAVLLRKLPLWYNPLQ NLADWLRLALGSANSAGVNIS TATVCRQCEDAPCANVCPNGAI SRDKGFVHVMQERCIGCKTCV VACPYGAMEVVVRPVIRNSGA GLNVRADKAEANKCDLCNHRE DGPACMAACPTHALICVDRNK LEQLSAEKRRRIPGNIRIRSGR YRRPVTA GCD AVVS GRAGYAI HDGGNNSMAKNTSCGVQLRIR GKVQGVGFRPFVWQLAQQLSH GSRMRDGTCLNKYDEYSRSGS MQYNPLGKTDLRVSRCLCLGCM TFGEPDRGNHAWTLPEESSRPII KRALEGGINFFDTANSYSDGSS EEIVGRALRDFARREDVVVATK VFHRVGDLPGLSRAQILRSIDD SLRRLGMDYVDILQIHRWDYN TPIETLEALNDVVKAGKARYI GASSMHASQFAQALELQKQHG WAQFVKSDENDAPDRQSGSTG SQCKNCGADTEPQVAAGPGLS ELNPVHCPHLHYRAHFRADRH SVACSLLDTPVTGHQVAPTYRQ QVPRAGQVHDPSKHTRMPCEN IDPVRTIIRISDPPVPASATLGA SKASRIRPRRSHSIPEITAKSRKP GGQPKWQVICWLDREKVVV MQTVRDQIGQHVFTAHRLDRP TSGVLLMGLSSEAGRLLAQQFE
26100	56468	A	26247	1	1833	
26101	56469	A	26248	1	517	MRNKLSFDLQLSARKAAIAERI AAHKIARSKVSVFLMAMSAGV FMAIGFTFYLSVIADAPSSQALT HLVGGLCFTLGFI LLAVCGTSLF TSSVMTVMAKSRGVISWRTWL INALLVACGNLAGIACFSLLIWF SGLVMSENAMWGVA VVYTA PR AKCIHLLNLSASALCAI
26102	56470	A	26249	3117	3527	EAVHRLARYRDAPRRS**SPLL CASVYP*LEQVPLQAQAVVPLR VLQAGKPVVPVAVLNAQAAAL ARPVAKLAAATAVQAAADRQ AAAPAALDAEHVA AVPALQAA AGPVDAAAQTHKAVGTGVAA TDEQPHAPER

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26095	56463	A	26242	1	2084	MLFPLATSGAMEPFPFLAGTAG ALVGGQLQNIQSGVLASLSAMLP QTGQPGVVDDLNGIVDRAVLA AAGDADVASGAARLSARHRSI VISSMGERCCFIRSRITRICGHWI CPQGNEIPVVAVASHDTASAVI ASPLNGSRAAYLSSGTWSLMG FESQTPFTNDTALAANITNEGG AEGRYRVLKNIMGLWLLQRVL QEQQINDLPALISATQALPACRF IINPNDDRFINPETMCSEIQAAC RETAQPIESDAELARCIFDSLA LLYADVLHELAQLRGEDFSQL HIVGGGCQNTLLNQLCADACGI RVIAGPVEASTLGNIGIQLMTLD ELNNVDDFRQVVSTTANLTTFT PNPDNSLYTTDKGALRMTTQL EQAWELAKQRF AAVGIDVEEA LRQLDRLPVSMHCWQGDDVSG FENPEGSLTGGIQTGNYPGKR VMPVSYVPIWNSTLSLSGSNWF NRKALGSPARYDVLPKWWRN VVKPTRTRYIGIAFYKVGEP KIEPDWMINGGVPELKKQLDL NDAVPEISGTILFREDYRNKPQT QQAADPPIRAKAAEIAVAHAH YLSIEFYRIVRIDPHAEFLSNEQ VERQLKSAMERWIINVLSAQIR PQPAVTHYRGLATVEMPVATG RYPTRY\GLVELEPKTGRKHQ LRRHLAHLRHPHIGDSKHGDLR QNRSGAEHFG LQRMER
26096	56464	A	26243	1	2871	
26097	56465	A	26244	690	824	
26098	56466	A	26245	950	1484	

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26091	56459	A	26238	732	1025	HEAKRTGRSYWFTAV*WLRG WRRMVARQNAKNCWHGTFFR VARVSLPISAHASSTHLSGSAH YVPPSAYRNSRRYSRGLCRCRV SSCDAATGVVVPQ
26092	56460	A	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP VWCDGSGGTSGDPQQRGSEC TG*QSRSQ*MRPVQPS*RRPGV YGGLPDS\WLICVDRNKLEQLT PEKRRQAKLRAMKPDEFAQIQ QAVITQMLQHPQTLGEEASKLS KDFDRGNMRFDSRDKIVAQIKL VTPQKLADFFHQAVVEPQGMA ILSQISGSQNGKAEYVHPEGWK VWENVSALQQTMLMSEKNEQ NLYDCGALFAPVTWTSGSAAF PRPLTVEELLVVTFTAATAEL RGRIRSNIHELRIACLRETTDNP LYERLLEEIDDKAQAAQWLLL AERQMDEAAVFTIHSFCQRM NLNTNECCFQRTTKTIHRDSFK STPRAAKSCSGLLPALAPSQISS NTPIQPLSRKFSGVTSPTSAA
26093	56461	A	26240	1	2235	
26094	56462	A	26241	166	416	CHVVGPFRVRRNLISAQH\PLTL NS\RH\TTTAAARLLRYFGTPR YRHSIDIHMQLDMTTSRSLSSL RDQLHCRWLLPAERQAI



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26089	56457	A	26236	530	1865	RGNKRLDLMFKQSHASMYIKQ PEQLDYQLNLKEVITAVFISMV VLNISPTLY/PDKPSPKDKYVAY AINIPDYELAADVYNINVTSPSG QQETFKILINLEHLRQTLEKSL TAVQKSQCEIITPKKPGEAILHA FNATYQQIRENMSEFARCHYG YIQIPPVTTFRADGPETPEEEKG YWFHAYQPEDLCTIHNPMGDL QDFIALVKDAKKFGNDIIPDYTF NFMGIGGGSGKNDLDYPSADIRA KISKDIEDPVTKERKQIHPEDIH LTAKDFEASKDNISKDEWENLH ALKEKRLNGMPKTTTPKSDQVI MLQNQYVREMRKYGVRLRY DAAKHSKHEQIERSITPPLKNY NERVHNTNLFNPKYHKKAVM NYMEYLVTCQLDEQQMSSLLY ERDDLSAIDFSLLMKTIKAFSFG GDLQTLASKPGSTISSIPSERRILI
26090	56458	A	26237	14	2031	LIVLS*QHG/DLRQNRSGAEHFG LQRLMLHASQLSLTHPFTGEPL TIHAGLDDTWMQALSQFGWRG LLPENERVEFSAPSGQDGDPTL GLIKEVACELSGMMRRSQPWE EAEESIPDRGESLLEVSGTPNAG WGAEGLAEREALLCCCCGPM GPDPLGLGSPGSVRGRSRLIHH AISGEALWEVTSEGLDMAAAR QFAIEKGAPALRAMTFIERAAM LKAVAKHLLSEKERFYALSAQT GATRADS WVDIEGGIGTLFTYA SLGSREL PDDTLWPEDELIPLSK EGGFAARHLLTSKSGVAVHINA FNFPCWGMLEKLAPTWSGRNA SHHQTSYRDGPLTQAMEFEDK AQRDVETARHFTFFRIIANED KKTGFPRFQTIVITASHKTIDRT RYTYGAWRCYRPLLTVVEEYRA TGSLITQPKFPPhKSSEVHRVPR NQGRFVAVNSTLPTEPATVAPV RGNASRD TAKTQTAERPSTTR PARQQA VIEPKKPQATVKTEPK PVAQTPKRTEPAAPVASTKAPA ATSTPAPKETATTAPVQTASPA QTTATPAAGAKTAGNVGSLKS APSSHYTLQLSSSSNYDNLNGW AKKENLKNYVVYETTRNGQP WYVLVSGVYASKEEAKKAVST LPADVQAKNPWAKPLRQRHRD LRGDERRDDRSEYFNRQVIS

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26086	56454	A	26233	152	2099	GNRLLVVSFIASFKNSTHFKGIF AMRIILLGAPGAGKGTQAQFIM EKYGIPQISTGDMRLAAVKSGS ELGKQAKDIMDAGKLVTDELV IALVKERIAQEDCRNGFLLDGF PRTIPQADAMKEAGINGHYVLE FDVPDELIVDRIVGRRVHAPSG RVYHVKFNPPKVEGKDDVTGE ELTTRKDDQEETVRKRLVEYH QMTAPLIGYYKEAEAGNTKY AKVDGTPQIYRGSLYVSDQIG HTIVNPDGVVDCDGRYGCLET VASLSALKKQARVWLKSQPV TQLDPEKLTTAQLIAAWQSGEP WITSWVDRSANAIGLSLYNFLN ILNINQIWLYGRSCAFGENWLN TIIRQTGFNPFDRDEGPSVKATQ IGFGQLSRAQQGVDLGNMIITS GQIPVNPKTGEVPADVAAQAR QSLDNVKAIVEAAGLKVGDIV KTTVFVKDLNDFAPVNATYEA FFTEHNATFPARSCVEVARLPK DVKIEIEAIAMLYTGYHYNDAP SAVRYPRGNASGVELTPLEKLP IGKGIVKRRGEKLAILNFGTLM PEAAKVAESLNATLVDMRFVK PLDEALILEMAASHEALVTVEE NAIMGAGSGVNEVLMAHRKP VPVLNIGLPDFFIPQGTQEEMRA ELGLDAAGMEAKIKAWLA
26087	56455	A	26234	935	1020	
26088	56456	A	26235	145	373	

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26079	56447	A	26226	102	1655	RKQMNYSCLKQLKVFVTVAQEK SFSRAGERIGLSQSAVSHSVKE LENHTGVRLLDRTTRAVVLT AGQPLALRLERLLDELNSTLRD TGRMGQQLSGK\VRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIVI DPGPVGDQLQCEAILSEPFLLCH RDSALAVEDYVPWQALQGAKL VLQDYASGSRPLIDAALARNGI QANIVQEIGHPA\TLFPMVAAGI GISILPALALPLEGSPLVVKRIT PVVERQLMLINVIQTLRF AFIFR LSRRQHFAKVTPLLHRHGDYF VFIGFDYGTANCSVAVMRDGK PHLLKMENDSTLLPSMLCAPTR EACGRVDVIEVSKSKVRKNTY AMRYVAGQPAERILPPGSFASI GQALPPGEPLSTEERJIRILVWNI YKQQRAEWLSVLKNYGKDAH LVLLQEAQTTPELVQFATANYL AADHVPAFVLPQHTSGVMTLS AAHPVYCCPLRERKPILRLAKS ALVTVYPIFPYLSNS
26080	56448	A	26227	159	290	
26081	56449	A	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL INNFGRIQHDP AIFHFQRNEAVP LWTVSAQEVKKDFTSGLRHGS VRGDL
26082	56450	A	26229	50	409	GYASQALILASIPAASRPSSARIS S*VPCGIKKSGRPMFSTGTGLR WAISTSFTPLPAPPIMAFSSTVTS ASWLAAISRINASSSGFTKRIST SVAFSDSATFAASSTNSRNAPPP VEM
26083	56451	A	26230	405	626	
26084	56452	A	26231	1	1528	
26085	56453	B	26232	1	1755	

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26072	56440	A	26219	213	407	TTCCCTNLSIPLANKYRSLSPQS DWRLSMPR*NRYVQKAPARAN KTSPMKAPPANIALGVNVAR
26073	56441	A	26220	1	1179	
26074	56442	A	26221	176	569	WPMRHTFSEAHAQAQRAGGKNP GHDTADYATNAVHTEDIAGIIH PQQAFEHGNAPQARQTSYHAD NQRAANPNVAAGWRHADQTG NRARTRPQQ*RLTTQRPFTEDP AKNCRRCDDHSIHKCQCRDFIR RAR
26075	56443	A	26222	1442	2309	
26076	56444	A	26223	155	2929	HLHWFVFSGWFTVTRLAFGEG NNFFGNINWLMLKNIELTAVM GSIYQYIHVAFQGSFACITVGLI VGALAERIRFSAVLIFVVVWLT LSYIPIAHMVWGGGLLASHGAL DFAGGTVVHINAAIAGLVGAY LIGKRVGFCKEAFKPHNLPVVF TGTAILYIGWGFNAGSAGTAN EIAALAFVNTVVATAAAILGWI FGEWALRGKPSLLGACSGAIAG LVGVTPACGYIGVGGALIIGVV AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	A	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE LENHTGVRLLDRTTREVVLTD AGQQLALRLERLLDELNSTLRD TGRMGQQLSGKVRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIVI DPGPVGDQLQCEAILSEPFLLCH RDSALAVEDYVPAALPLPEGSPL VVKRITPVVERQLMLVRRKNR SLSTAAEALWDVVRDQGNAL MAAA

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26066	56434	A	26213	1	899	MGRTRRDAAQAPGTRRSQDS RGYPYVTRPEGTDADDPQKDK AALGSHRVAGQPELFSIDELTR RDPHSASGAWTARYTVSTIAAF ALVIANRLYTIEEEATTPSGCGP ASSSTSSRGVDMCLRNLCMHG YDATIPLTLIAADSMDEYNKPD LSHVISQGRADDLTRQTAGEF AEQFNLHLFPQTWVTDIDAEAR VVKSQNNQWQYDKLVLATGA SAFVPPVPGRELMLTLNSQOEY RACETQLRDARRVLIVGGGLIG SELAMDFCAGKAVTLIDNAA SILASLMPPEVSSRLQHRLTEM GVHLLKSQLQGLEKTDSGIQA TLDRQRNIEVDAVIAATGLRPE TALARRAGLTINRGVCVDSYLQ TSNTDIYALGDCAEINGQRD*SS ARRVVPGRFPGAVRWRQLPHP LRYCAGGPALPECQNPFFPAPV TEISTADERPSPSTDAASGCLLP VALTTPEYWQRCRLA
26067	56435	A	26214	1	1264	MDYMPVPGMDWLCRETAGM RVSIIKGSVVFPLNPELVMKV RQRSTIVTPSGFKAGAFNFERFK EASNQTLGSTFLYSLSCPKNL GSQPLDFDTKKS YTLKVEAAN VHIDPRFSGRGPFKDTATVKIV VEDADEPPVFSSPTYLLEVHEN AALNSVIGQVTARDPDITSSPIR LYRIPGDDAKCVQFNREGVKA LKAKPVEKAAPAPAAAAPKAA PTPAKPMGEQLALYRMAGSNA DRIQGRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPMTRTKELAEV VAAATPVKDKFKHPATRTFQA VRIWVNSELEKIEQALKSSLNV LAPGGRLSIISFHSLEDRIKRF MRENSRGPQVPAGLPMTEEQL KKLGGRQLRALGKLMPGEEES VLRIAERTNA
26068	56436	B	26215	64	663	
26069	56437	A	26216	27	791	
26070	56438	B	26217	1	1638	
26071	56439	A	26218	1	375	STKKQRGEIHHPDGHGIAQDRH LPRTSVDQRPLRQTNHPAGL*Q ANG*GVFKRCRAHSATT**KDD E*NESAENAA*GGKVEGTDVT GDLLHENPAITPDKCEHNQATD CQWVALSCGRHERSSV

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26058	56426	A	26205	197	1043	YEKSLTMQQLQNIETAFERRA EITPANADTVTREAVNQVIAL DSGALRVAEKIDGQWVTHQWL KKAVLLSFRINDNQVIEGAESR YFDKVPMPKFADYDEARFQKEG FRV\PPAA\VRQGA\FIARNTVL MPSYVNIG\AYVDEGTMVDTW ATVGSQAQIGKNVHLSGGVGI GGVLEPLQANPTIIEDNCFIGAR SEVVEGVIVEEGSVISMGVYIG QSTRIDRETGEIHYGRVPAGS VVVSGNLPKDGKYSLYCAVIV KKVDAKTRGKVGINELLRTID
26059	56427	A	26206	1	406	MGKKNWNTLGEVVCSCRMFL PDANTLAKNSACSAASAVQAA DRPDSQEAEELEHMAHSRCAL RCQTLVIVHVSMLRVSWYHSVI IVVPLTEPLLESLVRCRLRSRRD DVPVAPAVSATPRREP\SVLRIA ERTNA
26060	56428	A	26207	1	2574	MWAFRGKRPVTLKILHVPITNL RKNITSTRGLTKESSQGLVRA QEEYTPAREIAKMG\GNPCRPG GIVFAGER*DVTSPYV*TSTRGL TKESSQGLVRAQEEYTPAREI AKMGWQSLPARRYCLCWRKIR RYITLRLNIAAYAGGYKAPVEDI ALWMETDGACDHVDFTWNIPS KCQGPMDIVSRPVFWAHGIV LFAGARNLNPTLTRIPPYLWLL TLRTGYAAAGMQALALDSRGS PDVVLTSTQHSEEIDQ
26061	56429	A	26208	1	3771	
26062	56430	A	26209	239	451	LPPTAWMSTTNLTSAMLSVRG NVPMTLPARRRVNLPSSLICTCF HKPA*RISMPKPVW*KARIISGN STS
26063	56431	A	26210	1	2079	
26064	56432	A	26211	1573	2562	
26065	56433	A	26212	275	643	SSRTALFTGSAVPGCAPPSGRSL FPQCLQSKLARSFPIRCRSGAA ILFRRLSFSPGTELILEDR/IVKRF MRENSRGQVPAGLPMTEEQ KLLGGRQLRALGKLMPEEE\S VLRIAERTNA

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26053	56421	A	26200	1	1236	MGPGDLPRGLATFWTELGLLS WARELARMPAVEMPPRSCPGR SRLSCSIGVAMFYGDLTAEQLY SRAISAAFTARHKGNQIQFFD PQQMEAAQKRLTEESDILNALE NHQFAIWLQPQVEMTSGKLP KSAAIMLPLSVNLSALQLMHPN MVADMLELLTRYRIQPGLILE VTESRRIDDPHAAVAILRPLRN AGVRVALDDFGMGYAGLRQL QHMKSLVRLTKSEVSSETDQDE LPLAKVSEVDEAKRQWLQGM HPVDTVTEPEPAEILAEFIRQHS AAGQLVARAVFLSPPYLVAEEE LSVLLESIKQNGDYADIACLTG SKDDYYYSTQAMSENYAAMSL QVVEQDIFSPIAHAVRFECQTY PRPYKVAMLMQAPYYFQEAQI EAAIAAMDVAPEYADIRQGIVG
26054	56422	A	26201	1	1161	
26055	56423	A	26202	1	1038	
26056	56424	A	26203	1	1472	MVRLCIRLPYVYAKVVDKNAL SLWMRERSDLWVQPKVDGVA VTLVYRDGKLNKAISRGNGLK GEDWTQKVSLSIAVPQTVSGPL ANSTLQGEIFLQREGHIQQQMG GINARAKVAGLMMRQDDSDTL NSLGVFVWAWPDGPQLMSDRL KELATAGFTLTQTYTRAVKNA DEVARVRNEWKAELPFVTD GVVVRAAKEPRIPPLATGPGRV AGGLEISTCSSGCRSEGNEPGKI SVVASLAPVMLDDKKVQRVNI GSVRRWQEWDIAPGDQILVSL AGQGIPRIDDVCPSDPAILSDIVP SW/VTTQW/LKKRAVSSRMMK NQ/VKKGSETGYFDKDEARFQK EGFRVPPAALRQGAFIARNT LRPSYVNIGAYVDEGTMVDTW ATVGSCAQIGKNVHLSAGVGIG GVLEPLQANPTIIEDNCFIGARS EVVEGVIVEEGSVISMGVYIGQ STRIYDRETGEIHYGRVP/AGKV DAKTRGKVGINELLRTID
26057	56425	A	26204	240	455	RLHPPYYRGWIFEEVPVISM YNGQSTRIYDR/ETGEIHYGRVP AGSVVVSIVDAKTRGKVGINE LLRTID

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26041	56409	A	26188	61	433	WIPHRGCRWSCLPVPRGALAF SPRVVSGTGRRGAEGGARRGG SGRTGAHGVGGRLRHGGLQVP SLAPREGSCTCGG\GSGAREEQ NLGFPREPRSGGGARGSDGICG MRVMFRKWILFCPSSR
26042	56410	A	26189	297	599	
26043	56411	A	26190	370	585	
26044	56412	A	26191	222	799	
26045	56413	A	26192	346	634	
26046	56414	B	26193	206	955	
26047	56415	A	26194	281	549	
26048	56416	A	26195	1981	2337	
26049	56417	A	26196	267	770	TRVDMIHVGLRKGPGETPS*SL RSFRAGQTGASRARGLTLLSSH SSALRKGGSPKHFCTLCWQTFLA WCVWKVAFSPSRCQTQFDLGK STQWTLEILTPKSHLFSRKQQ PQARAPAVFPAPLKGCHVGAR GSHCQGFQGCFRPSVAPLILGT DGFSLLEKLWTFKTC
26050	56418	A	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR SGKPFIDSTHSSHR*RQRNAVSL FSPVMSALRRCSVHRRLPDGGV VA
26051	56419	A	26198	357	981	HWRGDVLRSSHRTALQSRYP CGIYRSP/YKAR/MQIQFFDPQQ MEAAQKRLTEESDILNALENHQ FAIWLQPQVEMTSGKLRGISKQ LVGFTNRQNGATKLLVQYFTH RQIDCAGTADQNPAGKVDDC GVTGNVTDROQKQHGQAKE NELQNACAFQRAEEHKQRKYA PQTQVDTKELCIWRIGQTQFRH QQNRNQRAERTNHFGVR
26052	56420	A	26199	1	2601	



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26031	56399	A	26172	61	2560	PGFCHPRKAYSSYGQRSKGSQK MKASSGRCLVRWLQVLLPFL LSLFPGALPVQIRYSIPEELAKN SVVGNLAKDLGLSVRDL PARK LRVSAEKEYFTVNPESGDL LVS DRIDREQICGKQPLCVLDFDTV AENPLNIFYIAVIVQDINDNTPL FKQTKINLKIGESTKPGTTFPLD PALDSVGPNSLQRYHLNDNE YFDLAEKQTPDGRKYPELILKH SLDREEHSLHQLVLTAVDGGDP PQSGTTQIRIKVTDANDNPPVFS QDVYRVTLREDVPPGFFVLQVT ATDRDEGINAEITYSFHNVDEQ VKHFFNLNEKTGEITTKDDLDF EIASSTLSIEAKDPGDAAHCS IQVEILDDNDCAPEVIVTSVSTP LPEDSPPGTVIALIKTRDRDSGE NGEVYCQVLGNAKFILKSSSKN YYKLVTGDALDREEIPEYNLTI TATDGGKPPLSSSIIVTLHISDV NDNAPVVFQQTSYMVHVAENNP PGASIAQISASDPDLGPGSQVSY SIVASDLKPREILSYVSVAQSG VVFAQRAFDHEQLRAFELTLQ ARDQGSPALSANVSLRVLVGD LNDNAPRVLYPALGPDGSALFD MVPRAAEPGYLVTKVVAVDA DSGHNAWLSYHVLQASEPGLF SLGLRTGEVRTARALGDRDAA RQRLLVAVRDGGQPPLSATATL HLIFADSLQEVLPDLSDRREPSD
26032	56400	A	26179	47	325	ATMRLSVCLLLLTLALCCYRA NAVVCQALGSEITGFLLAGKPV FK\FQLAQFKAPVEAVASNMEA INCVDTM\AYEKRVLITKTLGKI AEKCDR
26033	56401	A	26180	1	3747	
26034	56402	A	26181	2776	2874	
26035	56403	A	26182	89	369	
26036	56404	A	26183	382	555	
26037	56405	A	26184	2	67	
26038	56406	B	26185	1	444	
26039	56407	A	26186	1129	1275	
26040	56408	A	26187	61	313	WIPHQGYRWSCLPVPRCALAFL SPWVVDGTGHRGAGGGAGWG GFGRGTGAHG\GVGGSGMAGCR SRAHSGGVGMTMTWQIPEVP

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26020	56388	A	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV NSPQVLL**GSGE/PRASDSPLP QLCGVSPHRPTWGSALWGGEQ CTSEMGETIDPPGPHTFSKNFCF ELQ
26021	56389	B	26162	1	453	
26022	56390	A	26163	1	379	
26023	56391	A	26164	1	1054	MFLQAAQKAWNPHLLLVRTQ AASTHGRADPHVGRCGETPQ SWGKGESLALAPLSLTKALED CSQISPSHQGTLECLLILDLRTG KLSLEHTEEPSDVPSHLLYRWSI SSAITEVFQALASSDSTSQPVNV HTKEDMKVQDIALVLP SRKSR NACRTTSTCKALLMRQLAAR VILQNCVSKSSRGHVPQKNLT LPVRGDSVLGSPHSRSLSAPP LPGLPLWRHLKSPSAHRCTVGG PFLGWPRPEPAPSACREALAAF P/PGQGS GPAAR\QPEPPPPWA PVQPESPRQAPPAPRSPVPSTT QGLRSTGTKHRDWQAAPPAAP VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLQ/IEVK MVS RTEANIDDSLIGGNASAEA PEGEGTESTVITGVDIVMNHHL QETSFTKEAYKKYIKDYMKSIK GKLEEQRPDRVKPFMTGAAEQI KHILANFKNYQ
26025	56393	A	26166	35	359	
26026	56394	A	26167	22	459	
26027	56395	B	26168	102	431	
26028	56396	A	26169	85	674	RRRLPSVAIMIILPGPSSSHDE MF\SDISKIR\EIADGVCAWKVE G\KMV\SRTE\GTID\DSLIGG\NA SAERPRGAKGTERHQLITGV\DI VMT\HL\QETKFSQKEASKK\YI K\DYMKSIKRET*KNRRPEKSK TFL*PGAAEQIKHILANFKNYQ FF\GENMNP\DGMMVALLDYP*D WV\TPYMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	A	26171	1	1527	

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26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAIIRWRRP TMNDTSFENCIKCTVCTTACPV SRVNPGYPGPKQAGPDGERLRL KD GALYDEALKYCINCKRCEV ACPSDVKIGDIIQRARAKYDTT RPSLRNFVLSHTDLMGSVSTPF APIVNTATSLKPVRQLLDAALK IDHRRTL PKYSFGTFRRWYRSV AAQQAQYKDQVAFFHGCFVN YNHPQLGKDLIKVLNAMGTGV QLLSKEKCCGVPLIANG\FTDK ARKQAITNVESIREAVGVKGIP VIATSSSTCTFALRDEYPEVLNV DNKGLRDHIELATRWLWRKLD EGKTLPLKPLPKVVYHTPCHM EKMGWTLTYLELLRNIPGLELT VLDSQCCGIAGTYGFKKENYPT SQAIGAPLFRQIEESGADLVVTD CETCKWQIEMSTSLRCEHPITLL
26017	56385	B	26158	1	2247	
26018	56386	A	26159	882	2372	HAVHESPPECRSNQQRPTRTCR TIIDIMEMYHALHVSWSNLQDQ QSIDERRVTFLGFDAATEARYL GYVRFMVNVEGRYTHFDAGTH GFNAQTPMWEKYQRMNLNVWH ACPRFLFDLDGTLVDSLPAVER AWSNWARRHGLAPEEVLAFIH GKQAITS LRHFMAGKSEADIAA EFTRLEHIEATETEGITALPGAIA LLSHLNKAASGVTNKGFLTVD EIRRVTRAFARLGTEKVRLTGG EPSLRRDFTDIIAAVREND AIRQ IAVTTNGYRLERDVASWRDAG LTGINVSVDSLDARQFHAITGQ DKFNQVMAGIDAAFEAGFEKV KVNTVLMRDVNHHLQDFTLN WIQHRPIQLRFIELMETGEGSEL FRKHHISGQVLRDELLRRGWIH QLRQRSDGPAQVFCHPDYAGEI GLIMPY\DKDF\CATCNRLRVSS IGKLHLCLFGEGGVNLRDLLED DTQQQALEARISAALREKKQTH FLHQNTTGITQNL SYIGG
26019	56387	A	26160	68	399	NKVKPRGDSV/PGSPHSPRLSP PPLPGLLLWR/PLEEPFSPPLHC GSPFLGWPRPGGRGLGG/PPHSE QPASLSLPPTPRAPVRPEPPRRA PPPAPRRPV PSTTQGLRNASAP

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26007	56375	A	26148	45	443	APSDP*KRDFPLPHGADSAMAE YDRCHRAVLSQGGQWPTALSA GDHAAAYSLHAALVQPERRCHG RCPVRNRLHAPVCPHIPG*RPAG SHHHHEFPFPPARAASTGPSIVQ DHQSLAGRSRRHDDPRHFGGC HHH
26008	56376	A	26149	581	957	TSWISFSRTTPSTVSPYSTVDAN GIIWSARNRLASVNNIASWLSFF SNPLYLAITKPNCRLLMMRNGCS TPGPGCWLSCIRC*WAVCSCVD AASRFLPCRGAARSASPHPPRQ APRRCGALW*PASAETNCSSPC SRLPS*LRGCCFKVLTLPGRSAI SQSTSTSASSALWRPLVAGIG
26009	56377	B	26150	1	3924	
26010	56378	A	26151	597	856	
26011	56379	B	26152	1	2781	
26012	56380	A	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR MPQHQTAYCRS*AWYRHVAH ERLPAQTDNRHQHADRWNG
26013	56381	B	26154	1	2802	
26014	56382	A	26155	4493	5470	IQRRNHRRDGWCLASLPAGTD HAGARAEAGSWHSGGPHRVR ARSVSTPFAPIVNTATSLKPVR QLLDAALKIDHRRRLPKYSFGT FRRWYRSVAAQQAQYKDQVA FFHGCFVNYNHPQLGQDLIKVL NAMGTGVQLLSKEKCCGVPLI ANGFTDKARKQAITNVESIREA VGVGIPVIATSSCTFALRDEY PEVLNVDNKGLRDHIELANRW LWRKLDEGQITLPLKPMTLKVV YHTPCHME*MGWTLY/TLELLR NIPGLE/LTVLDSQ/CC/GIPPIRV VIHMFRQIEESGADLVVTDCE CKWQIEMSTSLRCEHPITLLAQ ALA
26015	56383	A	26156	2467	3465	

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25995	56363	B	26136	4	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGDVQPSPTPRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138	1	734	SVHIGHQFFQFQSTSLNICPPLH RLFIAFQMNIIRRNAAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPFEANIGIHNVPIGF EAVIRQHFARRLNAFFALLFR PFRFLCFFPGINANQRSQVRQPQ LPRLDITFQFSWSLGGVDQRT VDIVCHQWRSALDRKEYYPAE TTMPTALHSRLCHVGKIKRPVI VLFREANQARVGLFE/H*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	A	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTGRQHFNNCAFTFRS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
26000	56368	A	26141	1	2469	
26001	56369	A	26142	1175	1435	
26002	56370	A	26143	218	443	AMARWKMLCTKSPPCVCLPGY PAG*RLAGPHHHHEFPPAGAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	A	26144	1	2031	
26004	56372	A	26145	1419	1875	TFCSPRSQPGSLKRRLRAGAGN CPLYSTGNGPLQRAICCAQPT*L HGRVPSHVPATFSSFQLWSFTV GACIHRSMYIISRSRCPDPKTK TATMLGITSFVMERCQLFILSRA FTSGQPTCYPTASSNTWFSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY PAG*RLAGPHHHHEFPPAGAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	A	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTPYWLIRTIC*KRRYD*K TRWYYAVAACLCNMGTTRKA NG

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25984	56352	A	26125	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTFFGVC TSASMNPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/WVAGTFD*SVWF GHDTDVVTLYRFHEALCYSVT LRTPHRRVLRFKSQHPGELACFI SPVA
25985	56353	A	26126	905	4761	PPHNWMPSNATPGIAFVWCAY GAI/LPGDAPVPVVDYRKVV KDTKGLIARWKYFWM SVIALG VAFALYLAGKDTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTGDLGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGS ALGGALGIIAVLLRQEFLLVIM GGVFVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25986	56354	A	26127	1056	1373	
25987	56355	A	26128	1	301	SSGTDAGR RYRPRQRPSKSRNN RRVNRQAPQQSSRN/SLRPSTT SSPFSLPVKLPAP/V*SAGMR LAEVRRVDSAISTVDSR*CPTAS SFSTGSITVT
25988	56356	A	26129	362	595	
25989	56357	B	26130	1	1305	
25990	56358	A	26131	1	2022	MISKRSERSFGYGVGLVRRQDF SSSEGFFNLHSLRIDINKCLGVRI STATSTMGIVLPEQIKLACNGIQ RVALCGDDYLTSDSFDVMF CSRFGWQVRPSSFCSPVFTWVT ENQQLHRGKDNLSLKNNSA CGAACGSLRGEKSDPPSARNNP SSQQGGKKESGQQPSLKDPHIL RHDSAHRPRKEKPRQPVNASLV VKFWRVKCVCVHNDHKRPACS VVCVDGDTYCWTEAYPAMGL PTLRGPDSALGERPE
25991	56359	A	26132	3	236	
25992	56360	B	26133	1	4638	
25993	56361	A	26134	1501	1914	SAFSRALTGRQHFNNCAFRFS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
25994	56362	A	26135	561	698	

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25980	56348	A	26121	1	1857	MRVCARACVTRTRTRMCVYAH TCVCVPTYAYVRVRVRVHVRA RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIHQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPALLLAFLCSTSPGF GDPDGLGVIAAYQDTPRPAAT AISELNALAVKGVILTGDNPRA AAAIAAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDRVRVAGSAGRYGGDGA GDSECVKIVAQEIRQTDRNIE DRSPRPSGERVRVRGKGGIEAN QPLSTAFTNQITIRQSIRLFSNQF VFHKGISRVVAGSSAISNVSPG CILRTPNCRRGFPISCTGEGKAA YGWQRDGGHAEYLLAEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDVY/V*IGVARVSWMNGRID SELRTRVRAYAHTRTRARTCTR TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
25981	56349	A	26122	3	1180	SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTA TQNLDIIRRYKAEYVILAGDHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKPANPPSPMPNDPSKS LASMGIYVFDADYLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPPPLSCVQSDPAEPLYAR CGYAGNFMESPRSGLRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITPGDPTRLHGSGFIDIR QIHHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQQYAARLRFQARGI SLQIAIHRVDIIHRFDVRQL
25982	56350	A	26123	16	543	
25983	56351	A	26124	1	3387	

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25976	56344	A	26117	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLDESGLFEWAALHVLRWG YGPGRLPFNRIGLIRTRIRQR LLFGLVTFILLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVIHSPG APDIREFTRDAIP
25977	56345	A	26118	5	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVTFLFHRI
25978	56346	A	26119	48	219	PETCGHLWAYVWPSCAAV\GL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	A	26120	1	912	



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25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPPDS WALDPGGGRARETPRGVSNAT KEPISVAQHGN/GGDKEIRRELK YYAHLGRRLKDWSGIPRYHGT VETDCGTGYVYDVIAFDGKP SITLTEFAEQCRYEEDIAQLRQL LKQLKRYLQDNRIVTMSLK PQ NILCHRISESEVIPVVCNIGEST LIPLATWSKWCCLRKQERLWK RFIAQPALAIALQKDLQPQATE ASGAENMASIASGNIARTDPDM LSIPLSKKICCFGDRIIEIPETIDQ PVRFWVL TGPVVD MGIYACYL SSPQWGWYAERDAE IENETVR REVEELRQASETDLQPGTIEYE RHRLTRAQADAQELKNARDSA E VVETAFCTFVLSRIAGEIASIL DGIPLSVQRRFPELENRHVDFL KRDIIKAMNKAALDELIPGLL SEYNRADRQYAGGSRVAARFA ASPRVAVLSVITGLIPRHVCAPY LLCGDPCCLSTPEDMTPRFRY AVRSGNRSTPGLDHRCDACQR SAYELADLRCRPPSTLFLLEA DKNDFSDALPAVADAMYAAPP RRKAAPSKPEKAVVSPLRSVRK ARHGVCSLRPDQYAVRNLP YRSCSSPDLQFMVWCALE
25966	56334	A	26107	1	2880	
25967	56335	B	26108	61	5101	
25968	56336	A	26109	80	561	IRPLPPRFKTESRSLPGCLQPGT FLWSRNRRLVGFPSMNGEDMG LLFLCSEWERSSEGWLCNREGG SGHSIEPHCCTFLHLTHRSLAFS LLAGVSCTCASSCKCKE\CKCTS CKKSECGAISRNGLWLKVGR EPKAVPEVRASGEPAFLCPCRL SLPV
25969	56337	A	26110	1	277	
25970	56338	A	26111	902	1006	
25971	56339	A	26112	2	1265	
25972	56340	A	26113	409	525	
25973	56341	A	26114	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPDKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRFQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL
25974	56342	A	26115	3	71	
25975	56343	A	26116	1	1212	

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25959	56327	A	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS FPGFNGDVHALNNVSLQINRGE IVGLVGESGSGKSVTAMLIMRL LPTGSYCVHRGQISLLGEDVLN AREKQLRQWRG/ARVAMIFQEP MTALNPTRRIALQMMDVIRHH QPISRREARAKAIDLLEEMQIPD AVEVMSRYPFELSGGMRQRVM IALAFSCEPQLIIADEPTTALDVT VQLQVLRLLKHKARASGTAVL FISHDMAVVSQLCDSVYV MYA GSVIESGVTADVIHHPRHPTIG LLQCAPEHGVP RQLLPAIPGTV PNLTHLPDGC AFRDRCYAAGA QCENVPALTACGDNNQRIGAC WYPQQEVISV
25960	56328	A	26101	3	102	ISRLNTQQHFG*RTRQISPHSPQ GCSRCPLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV MWSY*SPSPCR*PAGYRHMKL RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	A	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS* QRLLWSG*WSELCCSVPRQKR A

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25953	56321	A	26094	1	1260	AWARQDRRLSVKQWGKPPVD ETIPAKEQVRILRKLFDRYYGE VAGRGDGFCSPHVARYVGRVA G*RPCRLGPGHPTNRTPFVAPL LEALDIAKYFSVVIGDDVQNK KPHPDPLLLVAERMGIAPQQML FVGDSRNDIQAAKAAGCPSVG LTYGYNYGAEIDLSQPDVIYQSI NDLLPALGLPIAKIRNRKMTKPI VFSGAQPSGELTIGNYMGCTEA DRQFAFNFNFLIQLLTNGGP DRLGTTTPAGYTDLLVNYTYRI AFEGGGGQDFGLAAAIATLIFL LVAIMFPLLMVVAISLRQGNFA TGSLIPEQISWDHWKLALGFSV EQADGRITPPFPVLLWLWNSV KVAGISAIGIVALSTTCAYAFAR MRFP GKATLLKGMLIFQM FPA VLSLVALYALFAPRVRAALCY
25954	56322	A	26095	1	3240	
25955	56323	A	26096	494	792	ATRLRHGVTSVGDDGGLQLTV MDKLDVILLMSV/NPGFGGQSFI PQTLDKL/REVERRIDESGFDIR L/EVDGGVKVNNIGEIAA/AGA DMFVAGSAIFDQPDAR
25956	56324	A	26097	1624	2390	RTSERRWHAKALLKLSAHHA GFVCCKEEEERLATGKVGWLP VETLLAQQHIEGHYQVDPSLFK PNADCPVRVSGMSMKDIGIMD GDLLAVHKTQDVRNDPLLVP FTLIREGKLAANWPLEQDELLT RLQKSCDMTQVSADYNALFIG DECAVPPYRSAWVEGATEAEV RAFLSERGMPLADTPADHIGTL LLAASWLEDQSTEDESEALET FKRGA/LPKSLCLWGKAPAPHG SPVGGFSKGPKTWAPHEGAS
25957	56325	B	26098	1	534	
25958	56326	A	26099	67	399	

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25949	56317	B	26090	1	5073	
25950	56318	A	26091	249	531	CWAMRMDSKVGVITPIRMWSA SGPFAMGTLVPTFAAVTDIPTK SVTTCLRQICERWQAPSTR*SRF ASLSQPAPRFTSPITLALVLLP ARRC
25951	56319	A	26092	3	1038	LVLFGVAETYPVANDFAAGAG AYVRGRYAAGVRAWPTIITRK TMKTLVVALGGNALLQRGEAL TAENQYRNIA SAVPALARLARS YRLAIVHGNGPQVGLLALQNL AWKEVEPYPLDVLVAESQGM GYMLAQSLSAQPQMPPVTTVL TRIEVSPDDPAFLQPEKFIGPVY QPREEQEALEAAYGWQMKRDG KYLRRVVASPPQRKILDSEAIEL LLKEGHVVICSGGGGVPTND GAGESVIHKDLAAALLAEQIN ADGLVILTDADAVYENWGTPQ QRAIRHATPDELAPFAKADGSM GPNVTA VSGYVRSPVQMHRQ FQPVIIHIATNQIDHRRRIHHWL
25952	56320	A	26093	1	3639	MKRLIVGISGASGAIYGVRLQ VLRDVTDIETHLVMSQAARQT LSLETDFSLREVQALADVTHDA RDIAASISSGSFQTLGMVILPCSI KTL SGIVHSYTDGLLTRAADV LKERRPLVLCVRETPLHLGHLR LMTQAAEIGGNTGEIDEEEL LLYAIKGNVFNFTILHLPVA VQNDTIDFYQMFARIWSSHPQ WLTLYLAQHRAVIIPDDAKLHR NLLRWYSAGRLDIPELLDYAQS WRETEPDNEDAPY

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25945	56313	A	26086	1	1839	MRCQNA WWIMQHSSGSERLSS VLLHFRRTNLADSNDRIQYHSL RFFDEDGAQWLVLGDVLNHG PRNALPDGYAPRKVAERLNEV AHKVIAVRGNLRQRVDQMLLI SRAINRLVASNWNRRSAQMRC PISGKNLA WIPVQLPVYWQNN CRLLMRSHRKHGSGTNLPGE LMAIKLIAIDMDGTLLLPDHTIS PAVKNAIAAARARGVNVVLT GRPYAGVHNYLKEHMEQPGD YCITYNGALVQKAAD/GYDDY/ RF/LEKLSREVGSHFHALDRTT LYTANRDISYYTVHEFLRCHQ FPLVVCDDGGRMTPRAMFLFSSA HILMPLNYHNSHINTLFPVAGT LMVEPTESKVELDRFIDAML AIRAEIDQVKAGVWPLEDNPLV NAPHIQSELVAEWAHPYSREVA VFPAALVTGGSRGIGRATALL AQEGYTVAVNYQQLHAAQE VMNLITQAGGKAFVLQADISDE NQVVAMFTAIDQHDEPLAALV NNAGILFTQCTVENLTAERINR VLSTNVTGYFLCCREAVKRMA LKNGGSGGAIVNVSSVASRLGS PGEYVDYAASKGAIDTLTTGLS LEVAAQGIRVNCVRPGFIYTEM HASGGEAWTRRSR
25946	56314	A	26087	2	1275	VNFSKSSQIHHALRTVAGRFA VKSIDYFWHDSNASKRFHIWE SIMLELLFVIGYLVMLMVTGVS LLGIIAALVVATAIMFLGGMLA LMIKLLPWLLAISVVVVIKAI KAPKVPKYQRYDRWQLAVRRS PLLPDHTISPAVKNAIAAARAR GVNVVLTGRPYAGVHNYLKE LHMEQPGDYCITYNGAL/VYRK AAGWLAPLAAKLLKLMDLI GFLEKLSREVGSHFHALDRTTL YTANRDISYYTVHESFVATIPLV FCEAEKMDPNTQFLKVMIDE PAILDQAIARIPQEVKEKYPVLK APNLQQPHGSSGSSFHREIFFSS RSEDKRRGGLVVGISLLVVS GPWVRNANEPLGQLKTWFSLS HTLTLYTRAPACRLTSTQTEP RARPCLSPLSSEPRDRSLTPRLG QRFIYLAVQ
25947	56315	B	26088	1	1509	
25948	56316	A	26089	1	1323	

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25939	56307	A	26080	1429	2152	NLFREVVFPTHCPVCGSDVERV EGEAVARCTGALICGAQRKESL KHFVSRRAMDVDGMGDKIIDQ LVEKEYVHTPADLFLKLTAGKLT GLERMGPKSAQNVVNALEKAK ETTFARFLYALGIREVGEATAA GLAAYFGTLEALEAASIEELQK VPDVGIVVASHVHNFLPKKAT AMSSASCWRKVFTGLRRSLSTR KRLTARLLVKPWCLRAASGTP LKRASLLMFSGCFSHTSGLAMY
25940	56308	A	26081	1	2448	
25941	56309	A	26082	125	741	AHLNRTRWKVCWIR*RKISPW AKRNTKTVKG\WLAQLPAKYH QRATCMF\DRHGLLALLAGRFL AFVRTLLPTMAGISGLPNRRFQ FFNWLSGLLWVSVVTSFGYAL SMIPFVKRHEDQCRNGVFGKR KGGIAAALILTRLRRRFVSSWK RFRELRRKSSQADDMMNVFGILE DFTHQFIGGAFLRADISGAAKM SCLAKAQASSSMH
25942	56310	A	26083	1066	1359	
25943	56311	A	26084	256	952	RLKRCSTGKSMAVIQDIIAALW QHDFAAALADPHIVSVVYFVMF ATLFLENGLLPASFLPGDTLLIL AGALIAQGVMNFSGLRIAVLDP RNQVRGGGLSIFKGRWLGPNK TVKG\WLAQLPAKYHQQRATCM FDRHGLLALLAGRFLAFVRTLL PTMAGISGLPNRRFQFFNWLSG LLWVSVVTSFGYALSMIPFVKR HEDQVMTFLMILPIALLTAGLL GTLFVVIKKKYCNA
25944	56312	B	26085	1	1290	

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25936	56304	A	26077	1	2064	MNYSLKQLKVFVTVAQEKSF RAGERIGLSQSAVSHSVKELEN HTGVRLLDRTTREVVLTDAGQ QLAFRLERLLDELNNTLRDTGR YGATTERSARYSASLPAPTSGR SEPAALVQNSSSQPSSLKENIM KLRSVTYALFIAGLA AFSTFFLA AQSI RCGYETSQADSQHSGAK KFNDLLQERPKGELKLLFPDS TLGNAQAMISGVRGGTID\MEM SGSNYFAGLSPVMNLLDVPFLF RDTAHAKHTLDGKVGDDLKAS LEGKGLKVLAYWENGWRDVT NSRAPVKTPADLKGLKIRTNNS PMNIAAFKVFGA\NPI\MPFAE VYTGLETRTIDAQEHPI NVVWS AKFFE VQKFLSLTHHAYSPLL VINKAKFDGLSPEFQQALVSSA QEAGNYQRKLVAEDQQKIHDG MKEAGVEITDLDRKAFSDAL GNQVRDMFVKDVPQGADLLK AVDEPGWAERDIWAFAPAFFY PLFISDFNRVRLEFVGHYQDVC EKPASTTLWLDVGRSSGLDLTY QTLNVKNDLSHFPVPFFDPSDN RTNTLPMVFAGAPDVGLQQAS AIVASWFGSRSGWRGQNFV YNQLPDRNAIVFATNDKRPDFL RDHPAVKAPVIEMINHPQNPYV KLLVVFGRDDKDLLQAAKGIA QGNILFRGESVVVNEVKPLLPA GSQPVWSSSASESRCCFYA
25937	56305	A	26078	1	480	LGNTKTVKGWLAQLPAKYHQ RATCMFDRHGLLALLAGRFLA FVRTLLPTMAGISGLPNRRFQFF KAKLR\WLS*PTRIAAALAFMP/ FMDDHHPRLMQTVILQILQRRG TGDRLKIMVERRYAHVGFRCRQ LLDAQVFGVFILNPFQHAANQT EVSLATDQRQ
25938	56306	A	26079	1	2184	

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25927	56295	A	26068	3	373	VYTGLKPRTIDAQYTPINVV/W KFLSLTHHAYSPLLVVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQQKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQGADLLKAVDE
25928	56296	A	26069	1	1107	MGAFTGKTVLILGGSRGIGAAI VRRFVTDGANVRFTYAGSKDA AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISA FNSRASP K TPIAFTTRISNAPLL RTTSMATSLSALSVENTAVAPVS CARRLAASFDP A
25929	56297	A	26070	39	254	
25930	56298	A	26071	1432	1845	
25931	56299	A	26072	674	1614	AVIVVAILVSKSTGAWVAFSIR MPSITFSHNSVVAGVASARKDS SPSYGDPLESAIPKLNVKRSRSG LSKSLTLTSCSTIWITGQT PLKPCSVTGSVVPKAWRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPESATIRNDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIDSHLIRHRCVIYQWR QCLAQFRLNGWAASRSQSICRI GCD
25932	56300	A	26073	1	3476	MSSSCIEEVSPDDNWyRIANE LLSRAGIANGSAPADIRVKNPD FFKRVLQEGSLGLGESYMDGW WECDRLD MF FSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIVGKEHYDLGNDLFSRM LDPFMQYSCAYWKDADNLESA QQAKLK MICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYRDLNDQFDRIVSV GMFEHVGPKNYDTYFAVVDR
25933	56301	A	26074	200	1100	
25934	56302	A	26075	1	2061	
25935	56303	A	26076	1	3294	



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25914	56282	B	26055	319	3780	
25915	56283	A	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLSRMMRLQKEIRL
25917	56285	A	26058	662	1033	EPKRASGCMWPVGAHCHHPLL LLACQQKLGPPSHQASSRS*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLLFFTLHSY VAWPVEMMALNLLG
25918	56286	B	26059	1	2034	
25919	56287	A	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVSCSRGWKPEAT KAFMW
25920	56288	A	26061	352	2631	
25921	56289	B	26062	10	351	
25922	56290	A	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRYS IIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	A	26065	1348	1799	
25925	56293	A	26066	606	2219	ATYPSAHYPDHNERGEFLWPSL GLGKELDTFWSSLRVFGSPVSA VSRELVKFSLGGTV DSTGSLP VCGDISPVSDVA/ACTREPLRFR LQVGDRYITLMDLPGVGESGA RDTEYAALYREQLPRDLVLW LIKADDRALTVDHFYHQVIGE VYRHKVLFVISQSDKAEP TSGG GQLSTAQKQNI SRKICLLHEL FQ PVHPVCAVSVRLQWGLKVMA ERMIKCLPREATSPVVSQ LHPSF RTTVVREQARSDFGETVGAVL DSISAFPLIPAPVRAVIQAVRTT VVSFAASVTLLLLPLRSTPVEKS PTCILPASETFPLLVM LN PVAS LLTLTSPVLD TSCPTHSLSAAQP NLIQLSGNNNISFV VNR AVVTN VLNTMRTACNSQATI QIYNADI ARDFGTRGIFSINS GFSTVYSRRI GHQSPEVTGEAMALTSSQPSC IDDGLVAVNLD TDGLRIGDARQ KAITAGYPVVD TDDKCRIRRLR RIRHEQCADENSYQAYNYCRP VGRIRHLCRIRQSMPDATLSRLI
25926	56294	A	26067	543	741	

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25905	56273	A	26046	77	532	KPSRPEISKGKSVKPAASRRARE CAVQALYSWQLSQNDIADVEY QFLAEQDVKDQDVLYFRELLA GVATNTA\YLDGLMKPYLSRLL EELGQVEKAVLRJALYELSKRS DVPYKVAIKEAIELAKSFGAED SHKRVNGVLDKAAPVIRPNKK
25906	56274	A	26047	3	175	
25907	56275	A	26048	85	440	YSSSSLWAARKRRQMVLRSARR FATSDRVCRCLVWSAGTSRA KSKSTGWLSMASKAIGVSS*TK TPTARRVSSSLPCGMAIPLPIP VLPIFSRVRIASKTT*GSSLSCFA ARSLMTS
25908	56276	A	26049	80	706	KLIQVAVVIGGGQPLGAFLLCHG LAAEGYRFPVVDIQSDK\AANV AQEINAEYGESMAYGFGADAT SEQSVLALS RGVDEIFGRVDLL VYSAGIAKAAFISDFQLGDFDR SLQVNLVGYFLCAREFSRLMIR DGIQGRRIQINSKSGKVGSKHNS GYSAKFGGVGLTQSLALDLA EYGITVHSLMLGNLLKSPMFQS LLPQ*KTKLGIK
25909	56277	A	26050	741	893	TGCSGKRSLLQQRREERRRNPVQ KIRCTV*RVRNGRIRYCSPRAGF YSRYR
25910	56278	A	26051	269	987	
25911	56279	A	26052	1	1268	MDAKCDRSRFPWLWPTKRPRG CFATFVPIGIPYDQTKTHLHTLS LVAKRLADKTICRRLRAAQSD ELYQIITDTEGTPDEARCEEKQY MVLMI VSGRSGSGKSVALRAL EDMGFYCVDNLPVLLPDLAR TLADREISAASIDVRNMPESPE IFEQAMSNLPDAFSPQLFLDA DRNTLIRRYSDTRRLHPLSSKN LSLESAIDKESDLEPLHGFPDY DTVGFSCKRRIDYVCRIKHSRRI RQVLLNFAKSGAFSTTRGTDD KTRRSLLVTL/VAYFLCAR/EFS RM/MIR DGIHVRJIIQINSKSGKV GSKHNSGYSAKFGGVGLTQS LALDLAEYGITVHSLMLGNLLK SPMFQSLLPQYATKLGIPDQV EQYYIDKVPFKRGCDYQDVLN MLLFYASPKAISY\CTGQSINVT
25912	56280	A	26053	1	168	LKVFILVIFTLRSRE*EHAMFGFL FLC*FAENDGFQLHPCPKGHE LILFYGCIVFH
25913	56281	A	26054	2	253	

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25898	56266	A	26039	797	1440	PAMRLTAMRCISMKSRLPASR MQFCATVRWKYRCHREPTLSA QHGAFRSINPTPRNSRGNCWKK REMKWANWPIWCR*KN*RERS LSAICCASRK/TGQFVLPPARYH LRRSHSLRHGRRHTRKGERGTI NIVNGTPIHERSRNIDNRRSLGH WEGDLVSGGVGTGIVVTVGVII FTVINYGLTYIGVNPYWQYIIK GAIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLFALLPDTAEREEIRAGLS AKMSI/RAIATALNRSPSTISRE/ VQRNRGRYYKAVDAN/NRAN RMAKRPKCLLDQ/NLPLRKL LEKLNQHLRRSHS/LRHGRRHT RKGERGTIN/IVNGTPIHERSRNI DNSALVTVLR
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYTGMPADFRE FVFTIADKVGFAERIIILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGSMsAKGCCYDNACVE SFFHSLKVECIHGEHFISREIMR ATVFNYIECDYNRWRRHsWINS LLSQKRNTQGRIEDGRQH
25901	56269	B	26042	1	1048	
25902	56270	A	26043	323	1290	GTSMNTVGTPLLWGGFAVVVA IMLAIDLLLQRRGAHAMTMK QAAAWSLVWVTLsLLFNAAF WWYLVQTEGRAVADPQALAF LTGYLIEKSLAVDNVFWLML FSYFSVPAALQRRVLVYGVLG AIVLRTIMIFTGSWLISQFDWIL YIFGAFLFTGVKMALAHEDES GIGDK\RWcAGYA/VHLRMTDT IDNEHFFVRKNGLLYATPLMLV LILVELSDVIFAVDsIPAIFAVTT DPFIVLTSNLFAILGLRAMYFLL AGVTKRFSMLKYGLAGILVFIG IKRLIVNFNLLQTRACLGGGWA FGETLIIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045	1	777	

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25896	56264	A	26037	1162	3478	LVRFGLLPLAYSARCFARSSED RPKDECETCCIKYPNGRNVLSQ EIHQVFVLNGIQSMSGYVYNLG NELASMQGLVDVVRLSPQGSS AREAFSHSLDLARLAEKRGYH RYWLAEHNMGTGIAAATSVLI GYLAANTTTLHLGSGGVMLPN HSPLVIAEQFGTLNTLYPGRIDL GLGRAPGSDQRTMMALRRHM SGDIDNFPDVAELVDWFDAR DPILEPTHNGRRLCSTVRHPRM GYTPGVEPTTGPLGQGLANAV GLAIAERTLAAQFNQPDHEIVD HFTYVFMGDGCLMEEGWFTD DTAKRFEAYHWHVIHEIDGHD PQAVKEAILEAQSVKDKPSLIIC RTVIGFGSPNKAGKEEAHGAPL GEEVALARQKLGWHHPPEIP KEIYHAWDAREKGEKAQQSW NEKFAAYKKAHPQLAEFTRR MSGGLPKDWEKTTQKYINELQ ANPAKIATRKASQNTLNAYGP MLPELLGGSADLAPSNLTIWKG SVSLKEDPAGNYIHYGVRFG MTAIANGIAHHGGFVPYTATFL MFVEYARNAARMAALMKARQ IMVYTHDSIGLGEDGPTHQAVE QLASRLTPNFSTWRPCDQVEA AVGWKLAVRHNGPTALILSR QNLAQVERTPDQVKEIARGGY VLKDSGGKPDIIILATGSEIETL QAAEKLAGEGRNVVRVVSILASS
25897	56265	A	26038	1	1033	MNKSPKTRDIQEEELVLLLEE AAGGDEDREKEILIERIQSIKEE KQKGLGLAAGWTADVSSRRPG ASQLPPPPTHPIPYRGWGPPD QHLLSTLWTNVGSYKSGSFLQL GGWCMNLDMDLNSEESRWLF RRHWDTGGIKPKHERKRAVAHL TLSEREEIRAGLSAKMSIRAIAT ALNRSPSTISREVQRNRGRRYY KAVDANNRANRMAKRPKPLL DQNLPLRKLVLKLEMKWSPE QISGWLRRTKPRQKTLRISPETI YKTLYFRSREALNHLNIQVHLA RSHWLWPGERYNRNGERGPV TLWTG/TPISDGSRTSVKRALGQ WGEHLRRNAFFPLCATVV

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25889	56257	A	26030	1097	3332	TRVLVLDHRLRLCLYATVCAG ASWGMNPVVCSQQIDPQFHTM LMICASEEAQRMQQASEDEFN RALNIAFDNRLGLCKVESARQV FPLTGARYARQFASHRLALVGD AAHTIHLPLAGQGVNLGFMDDAA ELIAELKRLHRQGDIGQYIYL RRYERSRKHSALMLADSFVR TTHALRRSHGGFPRLLDAAAL RFANRRRTSCERNDDNTWSRSL YADLKNGTAQNIRAKFVFIGAG GAALKLLQESGIPEAKDYAGFP VGGQFLVSENPDVVNHHLAKV YGKASVGAPPMSVPHIDTRVL DGKRVVLFPGPFATFSTKFLKNG SLWDLMSSTTTSNVMPMMHV GLDNFDLVKYLVSQVMLSEED RFEALKEYYPQAKKEDWRLW QAGQRVQIIRDAEKGGLRL GTEVVSDQQGTIAALLGASPGA STAAPIMLNLLEKVFGRVSSP QWQATLKAIVPSYGRKLNGDV AATERERKTLHVIFNDLRPEQC EAGKSPSRVQLQWTNGGMLN APLSRLTLVEKLASMLDPGHL ALTQIAQHLALLQKMDHRQHS AFPELPQQAALYEWFSARCRW KEKALTQRGLLVQAGDQSEQIF TRWRAGAYNAWSLPGRCFIVL EELRWGAFGDACRLGSPQAVA LLGDLLEKATQHLEASINAAP TTRHYHQQWFASSTVPTGGEH
25890	56258	A	26031	115	654	HATQTMTPWFLYLIRTADNKL YTGITTDVERRYQQHQSGKGA KALTGGSARSPLIKKALAEQLP GIPIAGGDDFGSVTAGLAR*RF HQRHGPCWSMKAESLQLCRAD CQRRFQPMFSGGHFRHYRLSVC WRYRFIRPEHKTAFTARFPVDN RLGQMVAKPFHLLNATTGNIC GCFNTKRP
25891	56259	A	26032	1	348	
25892	56260	A	26033	1	906	
25893	56261	B	26034	59	910	
25894	56262	A	26035	1	3684	
25895	56263	A	26036	1	2634	

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25884	56252	A	26025	1	1488	
25885	56253	A	26026	1	1919	MNKAHFVSNLGATKCCPLSFLP YRWRRVIAFVVAFYFRHLIDLL VVQMHFKLVKGNVDVVFTAQ LIDSTVQLIDSTTTVTQFTHIQT QLMIQRAGTKCRKEDFRHCVGI LEPEWYPPIIVRVVVDVSQFEV RSQSLIFAVGEGITCIYTFITHA VVRLTVNFHVVAQLSSPDWNR PETLPVRSHVTSITQFEVVTGFG TEAPSVGVGATVNVSTVAHGC RQVVVEVRVAQATINKDVVRE VSRRVDVGS LAVLIHLTRTVIH VTFSEACSRDDPLSVVTVNFGI NTDHD AVNIIIVDGAVVAVEV TTEVAYPCAAVISQAMTRVGQ TSTNGVWTISSVNAFQIRTGAA RSLAPPWSLTEKVFCGTTMER MRAALEAIMPFTESSATQAPY LPCGREGLAVRQFFGRGEGIE TVAYLFRIRVVRTRVLSIGGFS RTRISSTPVKIATLRQNRSDCHA AMIADTYRQVTPDTPFSRHPFS RVLRLGLFFIIFKDKAHNGIGMI GGVNRADYLNLLKVFGLNDV SSPQWQATLKAIVPSYGRKLNG DVAATERELQYTSEVVGLNYD KPQAADNNRQHKVRAARSRRQ NRPDRGSQIADSTAGARCRFQT PTAGDGA*SAASTAPI/MLNLL EKVFGDRVSSPQWQATLKAIVP SYGRKLNGDVAATERELQYTS EVVGLNYDKPQAADNNRQHK
25886	56254	A	26027	1	2130	
25887	56255	A	26028	1144	1309	PGGSTPMAVEDPDFRSSERVLR FQPAVSVYGPEQPAV*DYAQTS YLRTPRRSDP
25888	56256	A	26029	1	3546	

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25876	56244	B	26017	1	3432	
25877	56245	A	26018	1385	2536	KSSQSHLITGMLEHVFKSGDT PSR/LPELMNGAQALANQINT/F VLNDADGAQAIQLGAN/HVWK LNGKPDDRMIED/YAGVMADTI RQHGADGL/VLLPNTRRGKLLA AKLPDASRTGETH/TVEWQAP AVAITRTATQARQSNSVDLDK ARLVSVVGRGITDSQTLRLYYI RLPPSLMGMRLTVFLLPICGFH RVGPPTLSVLATNRRNRNAKVF AHKNAPKFRSHTASEQWKSSIA HNKGVHPRVTSHTARHSLME TDIPHNIHSGHASPADITRHRQA VFNSVPKMASPIGDRVPTLHTQ HNSPANTGKAQSLLTCGPAAES CCRLIPRQMVSLVFRLLKARLLLI TTELPKGLVPVATISGTGNFGN TQSANPYRPSENTDLSLS
25878	56246	A	26019	926	1293	LSPNPKEPSCRTRLKKSGFTRI SAGAEPLMAIPARLSNSLACGA RDSAAKE/GFVVVPVCVAVEA DIAELDDEERDEFMADVGFIV GVKEVRAWTIPVGATAPQAAG KIHTDFEKGFIQAQT
25879	56247	A	26020	1	1278	
25880	56248	A	26021	678	1526	ERNNTNTCEVVPNRKRAYASHD MELSISPVGKGASKGEVNPADD IEVINTELALADLTCERAIHRV QKKAKGGDKDAKAEAVLEK CLAPQLENAGMLRALDLSAEEK AAIRYLSFLTTLKPTMYIANVNE DGFENNPYLDQVREIAAKEGSV VVPVCAAVEADIAELDDEERDE FMQELGLEEPGLNRVIRAGYKL LNLQTYFTAGVKEVRAWTIPV GATAPQAAGKIHTDFEKGFIQA QTISFEDFITYKGEQGAKEAGK MRAEGKDYIVKDGDMNLFN
25881	56249	A	26022	1177	1605	
25882	56250	A	26023	1	644	MDNHIALDFLLASECGSVYVY ATTHGRNMAGARALWRATGM TDADFGKPIIAVVNSFTQFVPG HVHLRDLGKLVAEQIEAAGGV AKEFNITIAVDDGIAMGHGGM YSLPSRELIADSVEYMVNAHCA DAMVCISNCDKITPGMLMASL RLNIPVIFVSGGPMAGTKLS DQIIKLDLVDAMIQGADPKIN/D YQSRGRRCPNRCFRCKNQAGS
25883	56251	B	26024	1	1944	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25871	56239	A	26012	1	1504	MGIVASASVQAAEIYNKDGK LDVYGKVKAMHYMSDNASKD GDQSYIRFGFKGETQINDQLTG YGRWEAEFAAWTDMFPEFGG DSSAQTDNFMTRASGLATYR KTTSSAYRWPELNLQYHRCTS AARAMLLSGRPVMQINERTAV RRQMTVYLRVERIHEIDPLVSL SHSMVIPIDVERPIAAAPCTPG LWRTKTPLRVPSTYPLRLPGA RVVCHRTFRLHLCKDWVFMFS GLLIILVPLIVGYLIPLRQQAAL KVINQLLSWMVYLILFFMGISL AFLDNPRPYLADSVDPDRQLLAP VNSISRYKTIEWLNYIATELHK GFTPLFRPDTPEEYKPTVRAHSE KKLQYVNEALKDEHWICQRF TIADAYLFTVLRWAYAVKLN EGLEHIAAFMQRMAERPEVQD ALSAEGLKGSRHLSAGARRLIL GIIVTFSLILALICVTQPFNPLAQ FIFLMLLWGVALIVRRMPGRFS ALMLIVLSLTVSCRYIWWRYTS TLNWDDPVS LVCGLILLFAETY AWIVLVLG YFQV V WPLNRQPV PLPKDMSLWPSVDIFVPTYNED LNVTPDELKQVLDVAAALKAL RAENISTKVFN SGLGISVFRDNS TRTRFSYASALNLLGLAQQLD EGKSQIAHGETVRETANMISFC ADAIGIRDDMYLGAGNAYMRE VGAALDDGYKQASGFSEPAMR
25872	56240	A	26013	2903	3024	
25873	56241	A	26014	123	335	
25874	56242	A	26015	2634	2787	
25875	56243	A	26016	1477	2485	NPEQLMVKTQRRVITPGEPAGI GPD LVVQLAQREWVELVCA DATLLTNRAAMLGLPLTLRPYS PNSPAQPQTAGTLTLLPVALRA PVTAGQLAVENGHYV VETLAR ACDGCLNGEFAALITGPGHKG VINDAGIPFTGHTFEERSQAK KVVMMLATEELRVGLATTHLP VRDIADAITPALLHEGIALHHD LRTKFGIGEPRI LVGGLNPHAG EGVPMGTTEEIDTIIPVLNELRA QGMKLNGLPADTLFQPKYLD NADAVRPMYHDQGLPVLKYQ GFGRGVNITLGLPFIRTSVDRGT ALELAGRGKADVGSFITALNL AIKMIVNTQ



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25870	56238	A	26011	2	1854	CGGTLARACDGLNGEFAA/LI TGPVHKGVINDAGI/PFTGHTF FEERSQAKK/VVMMLATEELRV ALATT/HLPLRDIADAITPALL/H QPKYLDNADAVLAMY/HDQGL PVLKYQGFGRGV/NITLGLPFIR TSVGHG/TALELAGRGQ/ADVG SFIRPYSAIK*L*NAGASVRWLS ERRICRAITGPVHKGVINDAGIP LPVIPSFSKSVRRRKRCDDAGD RRTSRGAGNDALPLRDIADAIT PALLHNRNILITPTPCWRCTRSG SSRAKIPGLRARCDITLGLPFIRT SVGHGQPLNWRDVANRCWQF YTPLFCHQMIVKPMHNRI PRAT YRGAVKSAIGLGCCCLKASATR CAYRWRRSGRRDQSRFRYFEIA GIRSRGINFIACPTCSRRNLMLS VRLTRWSNAWRYHSDGRFD YRLRGECPEALVSTLGVTGG NKKAASMKGMAQRPSGQQDM IDQLEARIRAKASQRTKRVELT FSRLKNNNVEKQDTALFALYQ RRLRCVRKVRRYVMAAVSAGC GGGVCAVSAYMPLNRLPNAQE ANNEYTSFENCIKCTVCTTACR VTLRNNDPKLPYLVKAGLKMK RVTRSPRRYCAAASATHRFNDE RAGKVQGMPDINKLPADRETC STLTCARSRQNQTNYPANRAA NAYQVVLATKALEKVSMKSP WQHKVSSPAAVRHLPSITQRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25866	56234	A	26007	3	417	
25867	56235	A	26008	507	717	WPEAEYLDNADAVLAMYPHD/Q GLPVLKYQGFGRGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	A	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RGLIHGTALT DHVG/ENGNYSSD*IHGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVFLHHPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITQLA
25869	56237	A	26010	1	469	MQKEYAYWMDGLKTCKPDNR KNALSNFGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQPRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLANARQKGIEKTCGTINKAG MPITT